



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 11830

TO: Nita M Minnifield
Location: rem-3c01/3c18
Art Unit: 1644
Tuesday, April 04, 2006

Case Serial Number: 09/942098

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Minnifield,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

*Reviewed
4/06*

THIS PAGE BLANK (USPTO)

183919

From: Chan, Christina
Sent: Monday, April 03, 2006 8:11 AM
To: Minnifield, Nita; STIC-Biotech/ChemLib
Subject: RE: rush interference sequence search

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

RECEIVED
APR - 3 2006
STIC-Biotech/ChemLib
(STIC)

-----Original Message-----

From: Minnifield, Nita
Sent: Monday, April 03, 2006 7:48 AM
To: Chan, Christina
Subject: rush interference sequence search

Christina,
Please approve, 2 month amdt. due.

STIC

09/942098

Please do an interference sequence search on SEQ ID NO: 1, 2, 30, and aa 187-203 of SEQ ID NO: 2 of this application.

Please do a commercial and interference sequence search on SEQ ID NO: 29, 90-93 and aa 191-202 of SEQ ID NO: 2 of this application.

Please provide a paper printout of all results.

Thanks,
Minnifield

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:23:07 ; Search time 1.03226 Seconds
(without alignments)
235.925 Million cell updates/sec

Title: US-09-942-098-1

Perfect score: 39

Sequence: 1 EANQATK 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pap.*
- 2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pap.*
- 3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pap.*
- 4: /SIDSS/ptodata/1/pubpaa/PCT_NEW PUB.pap.*
- 5: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pap.*
- 6: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pap.*
- 7: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pap.*
- 8: /SIDSS/ptodata/1/pubpaa/US60 NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	8	6	US-10-947-071-22
2	39	100.0	8	6	US-10-948-097-22
3	39	100.0	13	6	US-10-947-071-30
4	39	100.0	15	6	US-10-948-097-30
5	39	100.0	15	6	US-10-947-071-31
6	39	100.0	15	6	US-10-948-097-31
7	39	100.0	16	6	US-10-947-071-32
8	39	100.0	16	6	US-10-948-097-32
9	39	100.0	17	6	US-10-980-346B-6
10	39	100.0	17	6	US-10-980-346B-37
11	39	100.0	17	6	US-10-947-071-33
12	39	100.0	17	6	US-10-947-071-34
13	39	100.0	17	6	US-10-947-071-50
14	39	100.0	17	6	US-10-947-071-51
15	39	100.0	17	6	US-10-947-071-62
16	39	100.0	17	6	US-10-948-097-33
17	39	100.0	17	6	US-10-948-097-34
18	39	100.0	17	6	US-10-948-097-50
19	39	100.0	17	6	US-10-948-097-51
20	39	100.0	17	6	US-10-948-097-62
21	39	100.0	18	6	US-10-947-071-35
22	39	100.0	18	6	US-10-948-097-35
23	39	100.0	33	6	US-10-947-071-36
24	39	100.0	33	6	US-10-947-071-40
25	39	100.0	33	6	US-10-947-071-41

26	39	100.0	33	6	US-10-948-097-36	Sequence 16, Appl
27	39	100.0	33	6	US-10-948-097-40	Sequence 40, Appl
28	39	100.0	33	6	US-10-948-097-41	Sequence 41, Appl
29	39	100.0	116	7	US-11-195-098-11	Sequence 11, Appl
30	39	100.0	203	6	US-10-947-071-4	Sequence 4, Appl
31	39	100.0	203	6	US-10-948-097-4	Sequence 4, Appl
32	39	100.0	206	6	US-10-947-071-1	Sequence 1, Appl
33	39	100.0	206	6	US-10-947-071-2	Sequence 2, Appl
34	39	100.0	206	6	US-10-948-097-1	Sequence 1, Appl
35	39	100.0	206	6	US-10-948-097-2	Sequence 2, Appl
36	39	100.0	206	7	US-11-169-041-225	Sequence 225, Appl
37	39	100.0	334	6	US-10-947-071-20	Sequence 20, Appl
38	39	100.0	334	6	US-10-948-097-20	Sequence 20, Appl
39	36	92.3	17	6	US-10-980-346B-38	Sequence 38, Appl
40	36	92.3	17	6	US-10-947-071-61	Sequence 61, Appl
41	36	92.3	17	6	US-10-948-097-61	Sequence 61, Appl
42	36	92.3	22	6	US-10-980-346B-1	Sequence 1, Appl
43	36	92.3	24	7	US-11-195-098-8	Sequence 8, Appl
44	35	89.7	17	6	US-10-947-071-53	Sequence 53, Appl
45	35	89.7	17	6	US-10-947-071-55	Sequence 55, Appl

ALIGNMENTS

RESULT 1
US-10-947-071-22
; Sequence 22, Application US/10947071
; Publication No. US2006063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-947-071-22

Query Match 100.0%; Score 39; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EANQATK 8
|
Db 1 EANQATK 8

RESULT 2
US-10-948-097-22
; Sequence 22, Application US/10948097
; Publication No. US2006063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097

```
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-948-097-22

Query Match      100.0%; Score 39; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8
Db 1 EANORATK 8

RESULT 3
US-10-947-071-30
; Sequence 30, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-30

Query Match      100.0%; Score 39; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8
Db 5 EANORATK 12

RESULT 4
US-10-948-097-30
; Sequence 30, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-30

Query Match      100.0%; Score 39; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8
Db 5 EANORATK 12

RESULT 5
US-10-947-071-31
; Sequence 31, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-31

Query Match      100.0%; Score 39; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8
Db 8 EANORATK 15

RESULT 6
US-10-948-097-31
; Sequence 31, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-31

Query Match      100.0%; Score 39; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8
Db 8 EANORATK 15
```

```

; TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
; FILE REFERENCE: S-102,313
; CURRENT APPLICATION NUMBER: US/10/980,346B
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum
; OTHER INFORMATION: Neurotoxin (BoNT)
US-10-980-346B-6

Query Match      100.0%; Score 39; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EANQRATK 8
      |||||
DB      8 EANQRATK 15

RESULT 10
US-10-980-346B-37
; Sequence 37, Application US/10980346B
; Publication No. US20060024763A1
; GENERAL INFORMATION:
; APPLICANT: Los Alamos National Laboratory
; APPLICANT: Schmidt, Jurgen G., et al.
; TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
; TITLE OF INVENTION: of Botulinum Neurotoxins
; FILE REFERENCE: S-102,313
; CURRENT APPLICATION NUMBER: US/10/980,346B
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum
; OTHER INFORMATION: Neurotoxin (BoNT)
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(17)
; OTHER INFORMATION: amide bound at one end of the peptide
US-10-980-346B-37

Query Match      100.0%; Score 39; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EANQRATK 8
      |||||
DB      8 EANQRATK 15

RESULT 11
US-10-947-071-33
; Sequence 33, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity

```

```

; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-32

Query Match      100.0%; Score 39; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EANQRATK 8
      |||||
DB      8 EANQRATK 15

RESULT 8
US-10-948-097-32
; Sequence 32, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-32

Query Match      100.0%; Score 39; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EANQRATK 8
      |||||
DB      8 EANQRATK 15

RESULT 9
US-10-980-346B-6
; Sequence 6, Application US/10980346B
; Publication No. US20060024763A1
; GENERAL INFORMATION:
; APPLICANT: Los Alamos National Laboratory
; APPLICANT: Schmidt, Jurgen G., et al.

```

```
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-33

Query Match      100.0%; Score 39; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EANQRATK 8
Db      8 EANQRATK 15

RESULT 12
US-10-947-071-34
; Sequence 34, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-34

Query Match      100.0%; Score 39; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EANQRATK 8
Db      9 EANQRATK 16

RESULT 13
US-10-947-071-50
; Sequence 50, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-947-071-50

Query Match      100.0%; Score 39; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EANQRATK 8
Db      8 EANQRATK 15

RESULT 14
US-10-947-071-51
; Sequence 51, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; NAME/KEY: MOD_RES
; LOCATION: 16
; OTHER INFORMATION: Xaa=Nle
US-10-947-071-51

Query Match      100.0%; Score 39; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EANQRATK 8
Db      8 EANQRATK 15

RESULT 15
US-10-947-071-62
; Sequence 62, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-947-071-62
```

; OTHER INFORMATION: synthetic construct
US-10-947-071-62

Query Match 100.0%; Score 39; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EANORATK 8
| | | | |
Db 8 EANORATK 15

Search completed: April 3, 2006, 15:27:30
Job time : 1.03226 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:21:47 ; Search time 7.54839 Seconds
(without alignments)
442.828 Million cell updates/sec

Title: US-09-942-098-1
Perfect score: 39
Sequence: 1 EAMQRTK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	8	3	US-09-942-024-1
2	39	100.0	8	3	US-09-942-098-1
3	39	100.0	8	4	US-10-261-161-41
4	39	100.0	8	4	US-10-318-417-4
5	39	100.0	8	5	US-10-917-844-1
6	39	100.0	13	3	US-09-942-024-27
7	39	100.0	13	3	US-09-942-098-27
8	39	100.0	13	4	US-10-261-161-49
9	39	100.0	13	5	US-10-917-844-27
10	39	100.0	15	3	US-09-942-024-28
11	39	100.0	15	3	US-09-942-098-28
12	39	100.0	15	4	US-10-261-161-50
13	39	100.0	15	4	US-10-261-161-66
14	39	100.0	15	5	US-10-917-844-28
15	39	100.0	16	3	US-09-942-024-29
16	39	100.0	16	3	US-09-942-024-91
17	39	100.0	16	3	US-09-942-024-94
18	39	100.0	16	3	US-09-942-098-29
19	39	100.0	16	3	US-09-942-098-91
20	39	100.0	16	3	US-09-942-098-94
21	39	100.0	16	4	US-10-261-161-51
22	39	100.0	16	4	US-10-261-161-67
23	39	100.0	16	5	US-10-917-844-29
24	39	100.0	17	3	US-09-942-024-31
25	39	100.0	17	3	US-09-942-024-31
26	39	100.0	17	3	US-09-942-024-44
27	39	100.0	17	3	US-09-942-024-45

28	39	100.0	17	3	US-09-942-024-56	Sequence 56, Appl
29	39	100.0	17	3	US-09-942-098-30	Sequence 30, Appl
30	39	100.0	17	3	US-09-942-098-31	Sequence 31, Appl
31	39	100.0	17	3	US-09-942-098-44	Sequence 44, Appl
32	39	100.0	17	3	US-09-942-098-45	Sequence 45, Appl
33	39	100.0	17	3	US-09-942-098-56	Sequence 56, Appl
34	39	100.0	17	4	US-10-011-588-2	Sequence 2, Appl
35	39	100.0	17	4	US-10-261-161-52	Sequence 52, Appl
36	39	100.0	17	4	US-10-261-161-53	Sequence 53, Appl
37	39	100.0	17	4	US-10-261-161-68	Sequence 68, Appl
38	39	100.0	17	4	US-10-261-161-69	Sequence 69, Appl
39	39	100.0	17	4	US-10-261-161-70	Sequence 70, Appl
40	39	100.0	17	4	US-10-261-161-81	Sequence 81, Appl
41	39	100.0	17	5	US-10-917-844-30	Sequence 30, Appl
42	39	100.0	17	5	US-10-917-844-31	Sequence 31, Appl
43	39	100.0	17	5	US-10-917-844-44	Sequence 44, Appl
44	39	100.0	17	5	US-10-917-844-45	Sequence 45, Appl
45	39	100.0	17	5	US-10-917-844-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-09-942-024-1
; Sequence 1, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; TITLE OF INVENTION: Pret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-942-024-1

Query Match 100.0%; Score 39; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAMQRTK 8
Db 1 EAMQRTK 8
|||||||

RESULT 2
US-09-942-098-1
; Sequence 1, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Pret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-942-098-1

Query Match      100.0%; Score 39; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANQRATK 8
   |||||
Db 1 EANQRATK 8

RESULT 3
US-10-261-161-41
; Sequence 41, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-261-161-41

Query Match      100.0%; Score 39; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANQRATK 8
   |||||
Db 1 EANQRATK 8

RESULT 4
US-10-318-417-4
; Sequence 4, Application US/10318417
; Publication No. US20040115727A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Evolved Clostridial Toxins With Altered
; TITLE OF INVENTION: Protease Specificity
; FILE REFERENCE: P-AR 4670
; CURRENT APPLICATION NUMBER: US/10/318,417
; CURRENT FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-417-4

Query Match      100.0%; Score 39; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANQRATK 8
   |||||
Db 1 EANQRATK 8

US-09-942-098-1

RESULT 5
US-10-917-844-1
; Sequence 1, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
; APPLICANT: Aoki, Kei R.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
; FILE REFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917,844
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-917-844-1

Query Match      100.0%; Score 39; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANQRATK 8
   |||||
Db 1 EANQRATK 8

RESULT 6
US-09-942-024-27
; Sequence 27, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-27

Query Match      100.0%; Score 39; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANQRATK 8
   |||||
Db 5 EANQRATK 12

RESULT 7
US-09-942-098-27
; Sequence 27, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
```

```
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-27

Query Match      100.0%; Score 39; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EANQRATK 8
Db 5 EANQRATK 12

RESULT 8
US-10-261-161-49
; Sequence 49, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-49

Query Match      100.0%; Score 39; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EANQRATK 8
Db 5 EANQRATK 12

RESULT 9
US-10-917-844-27
; Sequence 27, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
; APPLICANT: Aoki, Kei R.
; TITLE OF INVENTION: GFP-SNAP25 Fluorescence Release Assay
; FILE REFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917,844
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 13
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-917-844-27

Query Match      100.0%; Score 39; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EANQRATK 8
Db 5 EANQRATK 12

RESULT 10
US-09-942-024-28
; Sequence 28, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-28

Query Match      100.0%; Score 39; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EANQRATK 8
Db 8 EANQRATK 15

RESULT 11
US-09-942-098-28
; Sequence 28, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-28

Query Match      100.0%; Score 39; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EANQRATK 8
Db 8 EANQRATK 15

RESULT 12
US-09-942-098-28
; Sequence 28, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-28

Query Match      100.0%; Score 39; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EANQRATK 8
Db 8 EANQRATK 15

RESULT 12
```

US-10-261-161-50
; Sequence 50, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-50

Query Match 100.0%; Score 39; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANQRATK 8
| | | | |
DB 8 EANQRATK 15

RESULT 13
US-10-261-161-66
; Sequence 66, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-261-161-66

Query Match 100.0%; Score 39; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANQRATK 8
| | | | |
DB 8 EANQRATK 15

RESULT 14
US-10-917-844-28
; Sequence 28, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
; APPLICANT: Aoki, Kei R.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
; FILE REFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917,844

; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-844-28

Query Match 100.0%; Score 39; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANQRATK 8
| | | | |
DB 8 EANQRATK 15

RESULT 15
US-09-942-024-29
; Sequence 29, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-29

Query Match 100.0%; Score 39; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANQRATK 8
| | | | |
DB 8 EANQRATK 15

Search completed: April 3, 2006, 15:26:53
Job time : 8.54839 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:16:44 ; Search time 2.12903 Seconds
(without alignments)
310.660 Million cell updates/sec

Title: US-09-942-098-1
Perfect score: 39
Sequence: 1 EANQRATK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTRUS COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	100.0	12	1 US-08-743-894B-41	Sequence 41, Appl
2	39	100.0	13	2 US-09-976-535A-1	Sequence 1, Appl
3	39	100.0	13	2 US-09-976-535A-11	Sequence 11, Appl
4	39	100.0	13	2 US-09-976-535A-12	Sequence 12, Appl
5	39	100.0	13	2 US-09-976-535A-13	Sequence 13, Appl
6	39	100.0	14	2 US-09-976-535A-2	Sequence 2, Appl
7	39	100.0	14	2 US-09-976-535A-6	Sequence 6, Appl
8	39	100.0	15	1 US-08-743-894B-38	Sequence 38, Appl
9	39	100.0	16	1 US-08-743-894B-49	Sequence 49, Appl
10	39	100.0	17	1 US-08-743-894B-1	Sequence 1, Appl
11	39	100.0	17	1 US-08-743-894B-19	Sequence 19, Appl
12	39	100.0	17	1 US-08-743-894B-24	Sequence 24, Appl
13	39	100.0	17	1 US-08-743-894B-28	Sequence 28, Appl
14	39	100.0	17	1 US-08-743-894B-36	Sequence 36, Appl
15	39	100.0	17	1 US-08-743-894B-37	Sequence 37, Appl
16	39	100.0	17	1 US-08-743-894B-50	Sequence 50, Appl
17	39	100.0	20	2 US-08-819-286-9	Sequence 9, Appl
18	39	100.0	26	2 US-08-819-286-8	Sequence 8, Appl
19	39	100.0	37	2 US-08-819-286-4	Sequence 4, Appl
20	39	100.0	70	1 US-08-760-001-10	Sequence 10, Appl
21	39	100.0	70	2 US-09-015-960-10	Sequence 10, Appl
22	39	100.0	70	2 US-09-534-572-10	Sequence 10, Appl
23	39	100.0	116	2 US-09-962-360B-11	Sequence 11, Appl
24	39	100.0	206	1 US-08-393-985-18	Sequence 18, Appl
25	39	100.0	206	2 US-08-819-286-1	Sequence 1, Appl
26	39	100.0	206	2 US-09-949-016-6311	Sequence 6311, Ap
27	39	100.0	219	2 US-09-949-016-10671	Sequence 10671, A

28	36	92.3	12	1	US-08-743-894B-17	Sequence 17, Appl
29	36	92.3	13	1	US-08-743-894B-16	Sequence 16, Appl
30	36	92.3	13	2	US-09-976-535A-9	Sequence 9, Appl
31	36	92.3	13	2	US-09-976-535A-14	Sequence 14, Appl
32	36	92.3	14	2	US-09-976-535A-7	Sequence 7, Appl
33	36	92.3	16	1	US-08-743-894B-7	Sequence 7, Appl
34	36	92.3	16	1	US-08-743-894B-51	Sequence 51, Appl
35	36	92.3	16	1	US-08-743-894B-52	Sequence 52, Appl
36	36	92.3	16	1	US-08-743-894B-53	Sequence 53, Appl
37	36	92.3	16	1	US-08-743-894B-54	Sequence 54, Appl
38	36	92.3	17	1	US-08-743-894B-2	Sequence 2, Appl
39	36	92.3	17	1	US-08-743-894B-4	Sequence 4, Appl
40	36	92.3	17	1	US-08-743-894B-6	Sequence 6, Appl
41	36	92.3	17	1	US-08-743-894B-18	Sequence 18, Appl
42	36	92.3	17	1	US-08-743-894B-21	Sequence 21, Appl
43	36	92.3	17	1	US-08-743-894B-23	Sequence 23, Appl
44	36	92.3	17	1	US-08-743-894B-43	Sequence 43, Appl
45	36	92.3	24	2	US-09-962-360B-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-743-894B-41
; Sequence 41, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSER: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: single
; TOPOLOGY: Linear
; FEATURE:
; US-08-743-894B-41

Query Match 100.0%; Score 39; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EANQRATK 8
|||||

Db 3 EANQRTK 10

RESULT 2

US-09-976-535A-1
; Sequence 1, Application US/09976535A
; Patent No. 6504006
; GENERAL INFORMATION:
; APPLICANT: Shine, Nancy R.
; APPLICANT: Crawford, Karen R.
; APPLICANT: Eaton, Linda J.
; TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol
; TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
; FILE REFERENCE: P010018
; CURRENT APPLICATION NUMBER: US/09/976,535A
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: human
US-09-976-535A-1

Query Match 100.0%; Score 39; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.083; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 1 EANQRTK 8
|||||

Db 5 EANQRTK 12

RESULT 3

US-09-976-535A-11
; Sequence 11, Application US/09976535A
; Patent No. 6504006
; GENERAL INFORMATION:
; APPLICANT: Shine, Nancy R.
; APPLICANT: Crawford, Karen R.
; APPLICANT: Eaton, Linda J.
; TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol
; TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
; FILE REFERENCE: P010018
; CURRENT APPLICATION NUMBER: US/09/976,535A
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: Xaa represents D-Arg
; NAME/KEY: misc feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Leu represents norleucine
US-09-976-535A-11

Query Match 100.0%; Score 39; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.083; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 1 EANQRTK 8
|||||

Db 5 EANQRTK 12

RESULT 4

US-09-976-535A-12

; Sequence 12, Application US/09976535A
; Patent No. 6504006
; GENERAL INFORMATION:
; APPLICANT: Shine, Nancy R.
; APPLICANT: Crawford, Karen R.
; APPLICANT: Eaton, Linda J.
; TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol
; TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
; FILE REFERENCE: P010018
; CURRENT APPLICATION NUMBER: US/09/976,535A
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 13
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: Xaa represents D-Arg
; NAME/KEY: misc feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Leu represents norleucine
US-09-976-535A-12

Query Match 100.0%; Score 39; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.083; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 1 EANQRTK 8
|||||

Db 5 EANQRTK 12

RESULT 5

US-09-976-535A-13
; Sequence 13, Application US/09976535A
; Patent No. 6504006
; GENERAL INFORMATION:
; APPLICANT: Shine, Nancy R.
; APPLICANT: Crawford, Karen R.
; APPLICANT: Eaton, Linda J.
; TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol
; TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
; FILE REFERENCE: P010018
; CURRENT APPLICATION NUMBER: US/09/976,535A
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: Xaa represents D-Arg
US-09-976-535A-13

Query Match 100.0%; Score 39; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.083; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 1 EANQRTK 8
|||||

Db 5 EANQRTK 12

RESULT 6

US-09-976-535A-2

```
; Sequence 2, Application US/09976535A
; Patent No. 6504006
; GENERAL INFORMATION:
; APPLICANT: Shine, Nancy R.
; APPLICANT: Crawford, Karen R.
; APPLICANT: Eaton, Linda J.
; TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol
; TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
; FILE REFERENCE: P010018
; CURRENT APPLICATION NUMBER: US/09/976,535A
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Leu represents norleucine
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa represents D-Lys
; US-09-976-535A-2

Query Match 100.0%; Score 39; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EANQRATK 8
Db 5 EANQRATK 12

RESULT 7
US-09-976-535A-6
; Sequence 6, Application US/09976535A
; Patent No. 6504006
; GENERAL INFORMATION:
; APPLICANT: Shine, Nancy R.
; APPLICANT: Crawford, Karen R.
; APPLICANT: Eaton, Linda J.
; TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol
; TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
; FILE REFERENCE: P010018
; CURRENT APPLICATION NUMBER: US/09/976,535A
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: Xaa represents D-Arg
; NAME/KEY: misc feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Leu represents norleucine
; US-09-976-535A-6

Query Match 100.0%; Score 39; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EANQRATK 8
Db 5 EANQRATK 12
```

RESULT 8

```
US-08-743-894B-38
; Sequence 38, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; US-08-743-894B-38

Query Match 100.0%; Score 39; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EANQRATK 8
Db 8 EANQRATK 15

RESULT 9
US-08-743-894B-49
; Sequence 49, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
```

OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
US-08-743-894B-49

Query Match 100.0%; Score 39; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANQRATK 8
Db 8 EANQRATK 15

RESULT 10
US-08-743-894B-1
Sequence 1, Application US/08743894B
Patent No. 5965699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MCMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence

STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-743-894B-1

Query Match 100.0%; Score 39; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANQRATK 8
Db 8 EANQRATK 15

RESULT 11
US-08-743-894B-19
Sequence 19, Application US/08743894B
Patent No. 5965699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MCMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
LOCATION: 4
OTHER INFORMATION: Xaa represents Abu, or 2-Aminobutyric Acid
US-08-743-894B-19

Query Match 100.0%; Score 39; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANQRATK 8
Db 8 EANQRATK 15

RESULT 12
US-08-743-894B-24
Sequence 24, Application US/08743894B
Patent No. 5965699
GENERAL INFORMATION:

APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MCMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 24:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
LOCATION: 16
OTHER INFORMATION: Xaa represents norleucine
US-08-743-894B-24

Query Match 100.0%; Score 39; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EANQRATK 8
| | | | |
Db 8 EANQRATK 15

RESULT 13
US-08-743-894B-28
Sequence 28, Application US/08743894B
Patent No. 5965699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MCMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B

FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
US-08-743-894B-28

Query Match 100.0%; Score 39; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EANQRATK 8
| | | | |
Db 8 EANQRATK 15

RESULT 14
US-08-743-894B-36
Sequence 36, Application US/08743894B
Patent No. 5965699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MCMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
US-08-743-894B-36

Query Match 100.0%; Score 39; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EAMQATK 8
 |||||
 Db 8 EAMQATK 15

RESULT 15
 US-08-743-894B-37
 ; Sequence 37, Application US/08743894B
 ; Patent No. 5965699
 ; GENERAL INFORMATION:
 ; APPLICANT: James J. Schmidt
 ; APPLICANT: Karen A. Bostian
 ; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
 ; STREET: USA MMCM - 504 Scott Street
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.0
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/743,894B
 ; FILING DATE: No. 5965699ember 6, 1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Charles H. Harris
 ; REGISTRATION NUMBER: 34,616
 ; REFERENCE/DOCKET NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 37:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 amino acids
 ; TYPE: amino acid sequence
 ; STRANDEDNESS: Single
 ; TOPOLOGY: Linear
 ; FEATURE:
 ;
 ; US-08-743-894B-37

Query Match 100.0%; Score 39; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EAMQATK 8
 |||||
 Db 8 EAMQATK 15

Search completed: April 3, 2006, 15:18:01
 Job time : 3.12903 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM protein - protein search, using sw model

Run on: April 3, 2006, 15:21:47 ; Search time 194.371 Seconds
(without alignments)
442.828 Million cell updates/sec

Title: US-09-942-098-2

Perfect score: 1048

Sequence: 1 MAEDADMNRLEEMQRRADQ.....SNKTRIDEANQRATKMLGSG 206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	206	3	US-09-942-024-2
2	1048	100.0	206	3	US-09-942-024-7
3	1048	100.0	206	3	US-09-942-024-12
4	1048	100.0	206	3	US-09-942-098-2
5	1048	100.0	206	3	US-09-942-098-7
6	1048	100.0	206	3	US-09-942-098-12
7	1048	100.0	206	4	US-10-261-161-4
8	1048	100.0	206	4	US-10-261-161-5
9	1048	100.0	206	4	US-10-261-161-109
10	1048	100.0	206	5	US-10-917-844-2
11	1048	100.0	206	5	US-10-917-844-12
12	1048	100.0	206	5	US-10-917-844-90
13	1004	95.8	206	4	US-10-318-417-3
14	1004	95.8	206	5	US-10-723-860-1223
15	1004	95.8	206	5	US-10-755-149-5012
16	933.5	89.1	203	3	US-09-942-024-14
17	933.5	89.1	203	3	US-09-942-098-14
18	933.5	89.1	203	4	US-10-261-161-7
19	933.5	89.1	203	5	US-09-917-844-14
20	895	85.4	249	3	US-09-942-024-16
21	895	85.4	249	3	US-09-942-098-16
22	895	85.4	249	4	US-10-261-161-9
23	895	85.4	249	5	US-10-917-844-16
24	627	59.8	212	3	US-09-942-024-15
25	627	59.8	212	3	US-09-942-098-15
26	627	59.8	212	4	US-10-261-161-8
27	627	59.8	212	5	US-10-917-844-15

28	625.5	59.7	212	6	US-11-097-143-20133	Sequence 20133, A
29	618.5	59.0	212	3	US-09-942-024-13	Sequence 13, Appl
30	618.5	59.0	212	3	US-09-942-098-13	Sequence 13, Appl
31	618.5	59.0	212	4	US-10-261-161-6	Sequence 6, Appl
32	618.5	59.0	212	5	US-10-917-844-13	Sequence 13, Appl
33	613.5	58.5	211	5	US-10-450-763-33306	Sequence 33306, A
34	609.5	58.2	211	4	US-10-318-417-1	Sequence 1, Appl
35	609.5	58.2	213	3	US-09-925-300-1718	Sequence 1718, Ap
36	578	55.2	116	3	US-09-962-360B-11	Sequence 11, Appl
37	578	55.2	116	4	US-10-802-574-11	Sequence 113, Appl
38	572	54.6	114	5	US-10-917-844-113	Sequence 12, Appl
39	572	54.6	116	3	US-09-962-360B-12	Sequence 12, Appl
40	572	54.6	116	4	US-10-802-574-12	Sequence 112, Appl
41	568	54.2	114	5	US-10-917-844-112	Sequence 2, Appl
42	512	48.9	158	4	US-10-318-417-2	Sequence 4, Appl
43	403	38.5	86	4	US-10-705-857-4	Sequence 1, Appl
44	391.5	37.4	82	4	US-10-705-857-1	Sequence 86, Appl
45	381	36.4	333	5	US-10-917-844-86	

ALIGNMENTS

RESULT 1
US-09-942-024-2
; Sequence 2, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-Ar 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; NUMBER OF SEQ ID NOS: 96
; CURRENT FILING DATE: 2001-08-28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-2

Qy	1	MAEDADMNRLEEMQRRADQ	100.0%;	Score 1048;	DB 3;	Length 206;
Db	1	MAEDADMNRLEEMQRRADQ	100.0%;	Pred. No. 1.2e-85;	Mismatches 0;	Indels 0; Gaps 0;
Qy	61	EGMDQINKDKAEKNTLDL	100.0%;	Score 1048;	DB 3;	Length 206;
Db	61	EGMDQINKDKAEKNTLDL	100.0%;	Pred. No. 1.2e-85;	Mismatches 0;	Indels 0; Gaps 0;
Qy	121	VDEEQMAISGGFTRRTND	100.0%;	Score 1048;	DB 3;	Length 206;
Db	121	VDEEQMAISGGFTRRTND	100.0%;	Pred. No. 1.2e-85;	Mismatches 0;	Indels 0; Gaps 0;
Qy	181	IMEKADSNKTRIDEANQR	100.0%;	Score 1048;	DB 3;	Length 206;
Db	181	IMEKADSNKTRIDEANQR	100.0%;	Pred. No. 1.2e-85;	Mismatches 0;	Indels 0; Gaps 0;

RESULT 2
US-09-942-024-7
; Sequence 7, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger

```
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-024-7

Query Match      100.0%; Score 1048; DB 3; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
Db 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
Qy 61 EEGMDQINKDMKEAEKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGVVASQPARV 120
Db 61 EEGMDQINKDMKEAEKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGVVASQPARV 120
Qy 121 VDREQWAISSGFFIRRVTTNDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTQNRQIDR 180
Db 121 VDREQWAISSGFFIRRVTTNDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTQNRQIDR 180
Qy 181 IMEKADSNKTRIDEANQATKMLGSG 206
Db 181 IMEKADSNKTRIDEANQATKMLGSG 206

RESULT 3
US-09-942-024-12
; Sequence 12, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: Serotype A/E Toxins
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-024-12

Query Match      100.0%; Score 1048; DB 3; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
Db 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
Qy 61 EEGMDQINKDMKEAEKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGVVASQPARV 120
Db 61 EEGMDQINKDMKEAEKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGVVASQPARV 120
Qy 121 VDREQWAISSGFFIRRVTTNDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTQNRQIDR 180
Db 121 VDREQWAISSGFFIRRVTTNDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTQNRQIDR 180
Qy 181 IMEKADSNKTRIDEANQATKMLGSG 206
Db 181 IMEKADSNKTRIDEANQATKMLGSG 206
```

```
Db 181 IMEKADSNKTRIDEANQATKMLGSG 206

RESULT 4
US-09-942-098-2
; Sequence 2, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-2

Query Match      100.0%; Score 1048; DB 3; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
Db 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
Qy 61 EEGMDQINKDMKEAEKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGVVASQPARV 120
Db 61 EEGMDQINKDMKEAEKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGVVASQPARV 120
Qy 121 VDREQWAISSGFFIRRVTTNDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTQNRQIDR 180
Db 121 VDREQWAISSGFFIRRVTTNDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTQNRQIDR 180
Qy 181 IMEKADSNKTRIDEANQATKMLGSG 206
Db 181 IMEKADSNKTRIDEANQATKMLGSG 206

RESULT 5
US-09-942-098-7
; Sequence 7, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-098-7

Query Match      100.0%; Score 1048; DB 3; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
Db 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
```

```

QY 61 ECGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAAGNNQDGVVASQPARV 120
    |||||||
DB 61 ECGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAAGNNQDGVVASQPARV 120
    |||||||
QY 121 VDREQMAISGGFIRRVTTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180
    |||||||
DB 121 VDREQMAISGGFIRRVTTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180
    |||||||
QY 181 IMEKADSNKTRIDEANQRATKMLGSG 206
    |||||||
DB 181 IMEKADSNKTRIDEANQRATKMLGSG 206
    |||||||

```

RESULT 6

```

US-09-942-098-12
; Sequence 12, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-12

```

```

Query Match 100.0%; Score 1048; DB 3; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
DB 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
    |||||||
QY 61 ECGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAAGNNQDGVVASQPARV 120
    |||||||
DB 61 ECGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAAGNNQDGVVASQPARV 120
    |||||||
QY 121 VDREQMAISGGFIRRVTTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180
    |||||||
DB 121 VDREQMAISGGFIRRVTTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180
    |||||||
QY 181 IMEKADSNKTRIDEANQRATKMLGSG 206
    |||||||
DB 181 IMEKADSNKTRIDEANQRATKMLGSG 206
    |||||||

```

RESULT 7

```

US-10-261-161-4
; Sequence 4, Application US/10261161
; Publication No. US2004007270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 206

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-4

Query Match 100.0%; Score 1048; DB 4; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
DB 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
    |||||||
QY 61 ECGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAAGNNQDGVVASQPARV 120
    |||||||
DB 61 ECGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAAGNNQDGVVASQPARV 120
    |||||||
QY 121 VDREQMAISGGFIRRVTTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180
    |||||||
DB 121 VDREQMAISGGFIRRVTTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180
    |||||||
QY 181 IMEKADSNKTRIDEANQRATKMLGSG 206
    |||||||
DB 181 IMEKADSNKTRIDEANQRATKMLGSG 206
    |||||||

```

RESULT 8

```

US-10-261-161-5
; Sequence 5, Application US/10261161
; Publication No. US2004007270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-261-161-5

```

```

Query Match 100.0%; Score 1048; DB 4; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
DB 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
    |||||||
QY 61 ECGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAAGNNQDGVVASQPARV 120
    |||||||
DB 61 ECGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAAGNNQDGVVASQPARV 120
    |||||||
QY 121 VDREQMAISGGFIRRVTTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180
    |||||||
DB 121 VDREQMAISGGFIRRVTTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180
    |||||||
QY 181 IMEKADSNKTRIDEANQRATKMLGSG 206
    |||||||
DB 181 IMEKADSNKTRIDEANQRATKMLGSG 206
    |||||||

```

RESULT 9

```

US-10-261-161-109
; Sequence 109, Application US/10261161
; Publication No. US2004007270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester

```

; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; FILE REFERENCE: Transfer (FRET) Assays For Clostridial Toxins
; CURRENT APPLICATION NUMBER: P-AR 4804
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-261-161-109

Query Match 100.0%; Score 1048; DB 4; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEDADNRNELEEMQRRADQADLESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
DB 1 MAEDADNRNELEEMQRRADQADLESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
QY 61 EEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQGVVASQPARV 120
DB 61 EEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQGVVASQPARV 120
QY 121 VDREQMAISGGFIRRTVDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTQNRQIDR 180
DB 121 VDREQMAISGGFIRRTVDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTQNRQIDR 180
QY 181 IMEKADSNKTRIDEANORATKMLGSG 206
DB 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 10
US-10-917-844-2
; Sequence 2, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei R.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; FILE REFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917,844
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-844-2

Query Match 100.0%; Score 1048; DB 5; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEDADNRNELEEMQRRADQADLESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
DB 1 MAEDADNRNELEEMQRRADQADLESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
QY 61 EEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQGVVASQPARV 120
DB 61 EEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQGVVASQPARV 120
QY 121 VDREQMAISGGFIRRTVDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTQNRQIDR 180

DB 121 VDREQMAISGGFIRRTVDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTQNRQIDR 180
QY 181 IMEKADSNKTRIDEANORATKMLGSG 206
DB 181 IMEKADSNKTRIDEANORATKMLGSG 206
RESULT 11
US-10-917-844-12
; Sequence 12, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
; APPLICANT: Aoki, Kei R.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; FILE REFERENCE: For Botulinum Neurotoxin Protease Activity
; CURRENT APPLICATION NUMBER: US/10/917,844
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-917-844-12

Query Match 100.0%; Score 1048; DB 5; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEDADNRNELEEMQRRADQADLESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
DB 1 MAEDADNRNELEEMQRRADQADLESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
QY 61 EEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQGVVASQPARV 120
DB 61 EEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQGVVASQPARV 120
QY 121 VDREQMAISGGFIRRTVDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTQNRQIDR 180
DB 121 VDREQMAISGGFIRRTVDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTQNRQIDR 180
QY 181 IMEKADSNKTRIDEANORATKMLGSG 206
DB 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 12
US-10-917-844-90
; Sequence 90, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
; APPLICANT: Aoki, Kei R.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; FILE REFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917,844
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

Db 181 IMEKADSNKTRIDEANQRATYMLGSG 206

Search completed: April 3, 2006, 15:26:52
Job time : 194.371 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:23:07 ; Search time 26.5806 Seconds

(without alignments)
235.925 Million cell updates/sec

Title: US-09-942-098-2

Perfect score: 1048

Sequence: 1 MAEDADNRNELEEMQRRADQ.....SNKTRIDEANQRATKMLGSG 206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pap.*
- 2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pap.*
- 3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pap.*
- 4: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pap.*
- 5: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pap.*
- 6: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pap.*
- 7: /SIDSS/ptodata/1/pubpaa/US12 NEW PUB.pap.*
- 8: /SIDSS/ptodata/1/pubpaa/US13 NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1048	100.0	206	6	US-10-947-071-1	Sequence 1, Appli
2	1048	100.0	206	6	US-10-947-071-2	Sequence 2, Appli
3	1048	100.0	206	6	US-10-948-097-1	Sequence 1, Appli
4	1048	100.0	206	6	US-10-948-097-2	Sequence 2, Appli
5	1048	100.0	206	7	US-11-169-041-225	Sequence 225, App
6	933.5	89.1	203	6	US-10-947-071-4	Sequence 4, Appli
7	933.5	89.1	203	6	US-10-948-097-4	Sequence 4, Appli
8	895	85.4	249	6	US-10-947-071-6	Sequence 6, Appli
9	895	85.4	249	6	US-10-948-097-6	Sequence 6, Appli
10	627	59.8	212	6	US-10-947-071-5	Sequence 5, Appli
11	627	59.8	212	6	US-10-948-097-5	Sequence 5, Appli
12	618.5	59.0	212	6	US-10-947-071-3	Sequence 3, Appli
13	618.5	59.0	212	6	US-10-948-097-3	Sequence 3, Appli
14	578	55.2	116	7	US-11-195-098-11	Sequence 11, Appli
15	572	54.6	116	7	US-11-195-098-12	Sequence 12, Appli
16	381	36.4	334	6	US-10-947-071-20	Sequence 20, Appli
17	381	36.4	334	6	US-10-948-097-20	Sequence 20, Appli
18	193	18.4	309	6	US-10-948-748-44	Sequence 44, Appli
19	164	15.6	33	6	US-10-947-071-36	Sequence 36, Appli
20	164	15.6	33	6	US-10-947-071-41	Sequence 41, Appli
21	164	15.6	33	6	US-10-948-097-36	Sequence 36, Appli
22	164	15.6	33	6	US-10-948-097-41	Sequence 41, Appli
23	158	15.1	31	6	US-10-980-346B-28	Sequence 28, Appli
24	155	14.8	33	6	US-10-947-071-40	Sequence 40, Appli
25	155	14.8	33	6	US-10-948-097-40	Sequence 40, Appli

26	129	12.3	25	6	US-10-980-346B-29	Sequence 29, Appli
27	129	12.3	25	6	US-10-980-346B-30	Sequence 30, Appli
28	129	12.3	25	6	US-10-980-346B-44	Sequence 44, Appli
29	109	10.4	232	7	US-10-467-962B-87	Sequence 87, Appli
30	108.5	10.4	587	7	US-11-096-568A-28248	Sequence 28248, A
31	107	10.2	30	6	US-10-947-071-42	Sequence 42, Appli
32	107	10.2	30	6	US-10-948-097-42	Sequence 42, Appli
33	106.5	10.2	1960	6	US-10-530-171-17	Sequence 17, Appli
34	106.5	10.2	1960	7	US-11-069-834-50	Sequence 50, Appli
35	105.5	10.1	1976	7	US-11-069-834-52	Sequence 52, Appli
36	105.5	10.1	1976	7	US-11-069-834-54	Sequence 54, Appli
37	105	10.0	1609	7	US-11-072-175-185	Sequence 185, App
38	104.5	10.0	1266	6	US-10-995-561-665	Sequence 665, App
39	104.5	10.0	1652	6	US-10-995-561-663	Sequence 663, App
40	104.5	10.0	1938	6	US-10-995-561-661	Sequence 661, App
41	104.5	10.0	1938	6	US-10-995-561-662	Sequence 662, App
42	104.5	10.0	1954	6	US-10-995-561-660	Sequence 660, App
43	104.5	10.0	1972	6	US-10-995-561-664	Sequence 664, App
44	104.5	10.0	1972	6	US-10-995-561-666	Sequence 666, App
45	104.5	10.0	2871	7	US-11-124-367A-264	Sequence 264, App

ALIGNMENTS

RESULT 1
US-10-947-071-1
; Sequence 1, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-1

Query Match	100.0%;	Score 1048;	DB 6;	Length 206;
Best Local Similarity	100.0%;	Pred. No. 6.4e-75;		
Matches 206;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	MAEDADNRNELEEMQRRADQ	LADESLSSTRMLQLVESKDAGIRTLVMDDEQGGQLERI	60
Db	1	MAEDADNRNELEEMQRRADQ	LADESLSSTRMLQLVESKDAGIRTLVMDDEQGGQLERI	60
Qy	61	EEGMDQINKMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKGANNQDGVASQPARV	120	
Db	61	EEGMDQINKMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKGANNQDGVASQPARV	120	
Qy	121	VDEREQMAISGGFIRRVNTDARENEMDNLEQVSGIIGNLRHMDMGNEIDTQNRQIDR	180	
Db	121	VDEREQMAISGGFIRRVNTDARENEMDNLEQVSGIIGNLRHMDMGNEIDTQNRQIDR	180	
Qy	181	IMEKADSNKTRIDEANQRATKMLGSG	206	
Db	181	IMEKADSNKTRIDEANQRATKMLGSG	206	

RESULT 2
US-10-947-071-2
; Sequence 2, Application US/10947071
; Publication No. US20060063221A1

```
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-947-071-2

Query Match      100.0%; Score 1048; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-75;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAEDADMRNELEEMORRADQLADESLESTRMLQVVEESKDAGIRTLVMLDDEQGEQLERI 60
Db      1 MAEDADMRNELEEMORRADQLADESLESTRMLQVVEESKDAGIRTLVMLDDEQGEQLERI 60

Qy      61 EEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGVVASQPARV 120
Db      61 EEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGVVASQPARV 120

Qy      121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMALDGMNEIDTONRQIDR 180
Db      121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMALDGMNEIDTONRQIDR 180

Qy      181 IMEKADSNKTRIDEANORATKMLGSG 206
Db      181 IMEKADSNKTRIDEANORATKMLGSG 206

Query Match      100.0%; Score 1048; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-75;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAEDADMRNELEEMORRADQLADESLESTRMLQVVEESKDAGIRTLVMLDDEQGEQLERI 60
Db      1 MAEDADMRNELEEMORRADQLADESLESTRMLQVVEESKDAGIRTLVMLDDEQGEQLERI 60

Qy      61 EEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGVVASQPARV 120
Db      61 EEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGVVASQPARV 120

Qy      121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMALDGMNEIDTONRQIDR 180
Db      121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMALDGMNEIDTONRQIDR 180

Qy      181 IMEKADSNKTRIDEANORATKMLGSG 206
Db      181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 3
US-10-948-097-1
; Sequence 1, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-1

Query Match      100.0%; Score 1048; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-75;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAEDADMRNELEEMORRADQLADESLESTRMLQVVEESKDAGIRTLVMLDDEQGEQLERI 60
Db      1 MAEDADMRNELEEMORRADQLADESLESTRMLQVVEESKDAGIRTLVMLDDEQGEQLERI 60

Qy      61 EEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGVVASQPARV 120
Db      61 EEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGVVASQPARV 120
```

```
61 EEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGVVASQPARV 120
121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMALDGMNEIDTONRQIDR 180
121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMALDGMNEIDTONRQIDR 180
181 IMEKADSNKTRIDEANORATKMLGSG 206
181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 4
US-10-948-097-2
; Sequence 2, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-948-097-2

Query Match      100.0%; Score 1048; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-75;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAEDADMRNELEEMORRADQLADESLESTRMLQVVEESKDAGIRTLVMLDDEQGEQLERI 60
Db      1 MAEDADMRNELEEMORRADQLADESLESTRMLQVVEESKDAGIRTLVMLDDEQGEQLERI 60

Qy      61 EEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGVVASQPARV 120
Db      61 EEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGVVASQPARV 120

Qy      121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMALDGMNEIDTONRQIDR 180
Db      121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMALDGMNEIDTONRQIDR 180

Qy      181 IMEKADSNKTRIDEANORATKMLGSG 206
Db      181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 5
US-11-169-041-225
; Sequence 225, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 225
```

```

; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-225

Query Match      100.0%; Score 1048; DB 7; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-75;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVESKDGAGIRTLVLMDEQGEQLERI 60
Db 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVESKDGAGIRTLVLMDEQGEQLERI 60

Qy 61 BEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAGNNDGVASQPARV 120
Db 61 BEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAGNNDGVASQPARV 120

Qy 121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180
Db 121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180

Qy 181 IMEKADSNKTRIDEANORATKMLGSG 206
Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 6
US-10-947-071-4
; Sequence 4, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-4

Query Match      89.1%; Score 933.5; DB 6; Length 203;
Best Local Similarity 89.3%; Pred. No. 5.3e-66;
Matches 184; Conservative 7; Mismatches 12; Indels 3; Gaps 1;

Qy 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVESKDGAGIRTLVLMDEQGEQLERI 60
Db 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVESKDGAGIRTLVLMDEQGEQLERI 60

Qy 61 BEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAGNNDGVASQPARV 120
Db 61 BEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAGNNDGVASQPARV 120

Qy 121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180
Db 121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180

Qy 181 IMEKADSNKTRIDEANORATKMLGSG 206
Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 7
US-10-948-097-4
; Sequence 4, Application US/10948097
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-4

Query Match      89.1%; Score 933.5; DB 6; Length 203;
Best Local Similarity 89.3%; Pred. No. 5.3e-66;
Matches 184; Conservative 7; Mismatches 12; Indels 3; Gaps 1;

Qy 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVESKDGAGIRTLVLMDEQGEQLERI 60
Db 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVESKDGAGIRTLVLMDEQGEQLERI 60

Qy 61 BEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAGNNDGVASQPARV 120
Db 61 BEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAGNNDGVASQPARV 120

Qy 121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180
Db 121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180

Qy 181 IMEKADSNKTRIDEANORATKMLGSG 206
Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 7
US-10-948-097-4
; Sequence 4, Application US/10948097
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-947-071-6

Query Match      85.4%; Score 895; DB 6; Length 249;
Best Local Similarity 95.1%; Pred. No. 6.8e-63;
Matches 175; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVESKDGAGIRTLVLMDEQGEQLERI 60
Db 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVESKDGAGIRTLVLMDEQGEQLERI 60

Qy 61 BEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAGNNDGVASQPARV 120

```

```

; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-4

Query Match      89.1%; Score 933.5; DB 6; Length 203;
Best Local Similarity 89.3%; Pred. No. 5.3e-66;
Matches 184; Conservative 7; Mismatches 12; Indels 3; Gaps 1;

Qy 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVESKDGAGIRTLVLMDEQGEQLERI 60
Db 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVESKDGAGIRTLVLMDEQGEQLERI 60

Qy 61 BEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAGNNDGVASQPARV 120
Db 61 BEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAGNNDGVASQPARV 120

Qy 121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180
Db 121 VDREQMAISGGFIRRVNTDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180

Qy 181 IMEKADSNKTRIDEANORATKMLGSG 206
Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 8
US-10-947-071-6
; Sequence 6, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-947-071-6

Query Match      85.4%; Score 895; DB 6; Length 249;
Best Local Similarity 95.1%; Pred. No. 6.8e-63;
Matches 175; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVESKDGAGIRTLVLMDEQGEQLERI 60
Db 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVESKDGAGIRTLVLMDEQGEQLERI 60

Qy 61 BEGMDQINKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAGNNDGVASQPARV 120

```

Db	Seq ID	Accession	Score	DB	Length	Mismatches	Conservative	Indels	Gaps
Db	61	EFGMNHINQDMKEAEKNLKDGLGKCCGLFICPCNKLKSSDAYKKAWGNQDGYVASQPARV	120						
Qy	121	VDEREQMAISGGFIRRVNTNDARENMENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR	180						
Db	121	VDEREQMAISGGFIRRVNTNDARENMENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR	180						
Qy	181	IMEK 184							
Db	181	IMEK 184							
RESULT 9									
US-10-948-097-6									
; Sequence 6, Application US/10948097									
; Publication No. US20060063222A1									
; GENERAL INFORMATION:									
; APPLICANT: Verhagen, Marc									
; APPLICANT: Williams, Dudley J.									
; APPLICANT: Gilmore, Marcella									
; APPLICANT: Steward, Lance									
; APPLICANT: Aoki, Kei Roger									
; TITLE OF INVENTION: Fluorescence Polarization Assays For									
; FILE REFERENCE: 66872-040									
; CURRENT APPLICATION NUMBER: US/10/948,097									
; CURRENT FILING DATE: 2004-09-22									
; NUMBER OF SEQ ID NOS: 96									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 6									
; LENGTH: 249									
; TYPE: PRT									
; ORGANISM: Gallus gallus									
US-10-948-097-6									
Query Match 85.4%; Score 895; DB 6; Length 249;									
Best Local Similarity 95.1%; Pred. No. 6.8e-63;									
Matches 175; Conservative 5; Mismatches 4; Indels 0; Gaps 0									
Qy	1	MAEDADMRNELEEMORRADQADLESLESTRMLQLVESKDAGIRTLVMLDEQGQLERI	60						
Db	1	MAEDADMRNELEEMORRADQADLESLESTRMLQLVESKDAGIRTLVMLDEQGQLDVR	60						
Qy	61	BEGMDQINKDMKEAEKNLTDLGKFCGLVCPCNKLKSSDAYKKAWGNQDGYVASQPARV	120						
Db	61	BEGMNHINQDMKEAEKNLKDGLGKCCGLFICPCNKLKSSDAYKKAWGNQDGYVASQPARV	120						
Qy	121	VDEREQMAISGGFIRRVNTNDARENMENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR	180						
Db	121	VDEREQMAISGGFIRRVNTNDARENMENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR	180						
Qy	181	IMEK 184							
Db	181	IMEK 184							
RESULT 10									
US-10-947-071-5									
; Sequence 5, Application US/10947071									
; Publication No. US20060063221A1									
; GENERAL INFORMATION:									
; APPLICANT: Williams, Dudley J.									
; APPLICANT: Gilmore, Marcella									
; APPLICANT: Steward, Lance									
; APPLICANT: Verhagen, Marc									
; APPLICANT: Aoki, Kei Roger									
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods									
; FILE REFERENCE: 66872-043									
; CURRENT APPLICATION NUMBER: US/10/947,071									
; CURRENT FILING DATE: 2004-09-21									
; NUMBER OF SEQ ID NOS: 101									
; SOFTWARE: FastSeq for Windows Version 4.0									

```

; Sequence 3, Application US/10947071
; Publication No. US2006063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Drosophila sp.
US-10-947-071-3

```

```

Query Match      59.0%; Score 618.5; DB 6; Length 212;
Best Local Similarity 62.9%; Pred. No. 2e-41;
Matches 124; Conservative 29; Mismatches 43; Indels 1; Gaps 1;

Qy 8 RNELEEMORRADQADLESLESTRMLQLVVEESKDAGIRTLVMLDQGEQLERIEEGMDQI 67
Db 15 KTELEELQINAGQVADESLESTRMLALCEEKAGIRTLVALDDQGEQLERIEEGMDQI 74

Qy 68 NKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKAWGNQDG-VVASQPARVVDEREQ 126
Db 75 NADMREAEKNLSGMEKCCGICVLPCKNSQSFKEDDGTWKGNDDGKVYNNQPVMDRRNG 134

Qy 127 MAISGGFIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDRIMEKAD 186
Db 135 MMAQAGYIGRITNDAREDEENMGQVNTMIGNLRNMLDMGSELENQNRQIDRINKKE 194

Qy 187 SNKTRIDEANORATKML 203
Db 195 SNEARIATANORAHQLL 211

```

```

RESULT 13
US-10-948-097-3
; Sequence 3, Application US/10948097
; Publication No. US2006063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Drosophila sp.
US-10-948-097-3

```

```

Query Match      59.0%; Score 618.5; DB 6; Length 212;
Best Local Similarity 62.9%; Pred. No. 2e-41;
Matches 124; Conservative 29; Mismatches 43; Indels 1; Gaps 1;

Qy 8 RNELEEMORRADQADLESLESTRMLQLVVEESKDAGIRTLVMLDQGEQLERIEEGMDQI 67
Db 15 KTELEELQINAGQVADESLESTRMLALCEEKAGIRTLVALDDQGEQLERIEEGMDQI 74

```

```

Qy 68 NKDMKEAKNLTDLGKFCGLVCPCNKLKSSDAYKAWGNQDG-VVASQPARVVDEREQ 126
Db 75 NADMREAEKNLSGMEKCCGICVLPCKNSQSFKEDDGTWKGNDDGKVYNNQPVMDRRNG 134

Qy 127 MAISGGFIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDRIMEKAD 186
Db 135 MMAQAGYIGRITNDAREDEENMGQVNTMIGNLRNMLDMGSELENQNRQIDRINKKE 194

Qy 187 SNKTRIDEANORATKML 203
Db 195 SNEARIATANORAHQLL 211

```

```

RESULT 14
US-11-195-098-11
; Sequence 11, Application US/11195098
; Publication No. US20050287622A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; FILE REFERENCE: 003/224/SAP
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/11/195,098
; PRIOR FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 09/962,360
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-11-195-098-11

```

```

Query Match      55.2%; Score 578; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.4e-38;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 93 NKLKSSDAYKAWGNQDGVVASQPARVVDEREQMAISGGFIRVTNDARENEMDENLEQ 152
Db 2 NKLKSSDAYKAWGNQDGVVASQPARVVDEREQMAISGGFIRVTNDARENEMDENLEQ 61

Qy 153 VSGIIGNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 206
Db 62 VSGIIGNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 115

```

```

RESULT 15
US-11-195-098-12
; Sequence 12, Application US/11195098
; Publication No. US20050287622A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Schmidt, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; FILE REFERENCE: 003/224/SAP
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/11/195,098
; PRIOR FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 09/962,360

```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:16:44 ; Search time 54.8226 Seconds
(without alignments)

310.660 Million cell updates/sec

Title: US-09-942-098-2

Perfect score: 1048

Sequence: 1 MAEDADMELEEMORRADO.....SNKTRIDEANQRATKMLGSG 206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H-COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCRU5-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	206	1	US-08-393-985-18
2	1048	100.0	206	2	US-08-819-286-1
3	1048	100.0	206	2	US-09-949-016-6311
4	1048	100.0	219	2	US-09-949-016-10671
5	578	55.2	116	2	US-09-962-360B-11
6	572	54.6	116	2	US-09-962-360B-12
7	512	48.9	158	2	US-09-949-016-10399
8	451	43.0	106	2	US-09-513-999C-7906
9	451	43.0	106	2	US-09-513-999C-7907
10	353	33.7	70	1	US-08-760-001-10
11	353	33.7	70	2	US-09-015-960-10
12	353	33.7	70	2	US-09-534-572-10
13	310	29.6	64	2	US-09-513-999C-4845
14	277	26.4	68	2	US-09-621-976-7614
15	230	21.9	300	2	US-09-952-689-9
16	197.5	18.8	284	2	US-09-952-689-3
17	184	17.6	37	2	US-08-819-286-4
18	183.5	17.5	283	2	US-09-952-689-5
19	166	15.8	282	2	US-09-949-016-10848
20	163.5	15.6	297	2	US-09-270-767-44925
21	155	14.8	303	2	US-09-952-689-7
22	137.5	13.1	1886	2	US-08-938-105-3
23	137.5	13.1	1935	2	US-09-538-092-916
24	137.5	13.1	1944	2	US-09-949-016-10929
25	136	13.0	1937	2	US-09-538-092-918
26	132	12.6	1939	2	US-09-538-092-915
27	132	12.6	1939	2	US-09-949-016-11104

28 131.5 12.5 1940 2 US-09-538-092-901 Sequence 901, App
29 131.5 12.5 1963 2 US-09-949-016-8888 Sequence 8888, Ap
30 131 12.5 1942 2 US-09-949-016-8135 Sequence 8135, Ap
31 130.5 12.5 1939 2 US-09-310-187A-1 Sequence 1, Appli
32 129.5 12.4 1939 2 US-09-538-092-917 Sequence 917, App
33 128 12.2 26 2 US-08-819-286-8 Sequence 8, Appli
34 125 11.9 1938 2 US-09-949-016-6417 Sequence 6417, Ap
35 125 11.9 1959 2 US-09-949-016-8134 Sequence 8134, Ap
36 124 11.8 1939 2 US-09-949-016-6925 Sequence 6925, Ap
37 117 11.2 200 2 US-09-949-016-9499 Sequence 9499, Ap
38 111.5 10.6 1972 2 US-08-875-435B-3 Sequence 3, Appli
39 111 10.6 1270 2 US-09-538-092-1321 Sequence 1321, Ap
40 107.5 10.3 1960 2 US-09-949-016-10872 Sequence 10872, A
41 107 10.2 1972 2 US-08-875-435B-4 Sequence 4, Appli
42 106.5 10.2 1960 2 US-09-538-092-1077 Sequence 1077, Ap
43 106 10.1 284 2 US-09-914-259-59 Sequence 59, Appl
44 106 10.1 284 2 US-09-914-259-60 Sequence 60, Appl
45 105.5 10.1 245 2 US-09-914-259-44 Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Scheller, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38, 615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-393-985-18

Query Match 100.0%; Score 1048; DB 1; Length 206;

Best Local Similarity 100.0%; Pred. No. 2.4e-97;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEDADMELEEMORRADOQLADESLESTRMLQVVEESKDAGINTLVMLDEQGQLERI 60
DB 1 MAEDADMELEEMORRADOQLADESLESTRMLQVVEESKDAGINTLVMLDEQGQLERI 60
QY 61 EFGMDQINKMKEAKNKJTDLKGKFCGLVCPCNKLKSSDAYKANNQDGVVASOPARV 120

Db 61 BEGMDQINKDMKEAEKNLTDLGKFCGLVCPCNKLKSSDAYKKAAGNNQGVVASQPARV 120
Qy 121 VDREQMAISGGFIRRTVNDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTONRQIDR 180
Db 121 VDREQMAISGGFIRRTVNDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTONRQIDR 180
Qy 181 IMEKADSNKTRIDEANORATKMLGSG 206
Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 2
; Sequence 1, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-1

Query Match 100.0%; Score 1048; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.4e-97;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAEDADMRNELEEMQRRADQLADESLSTRMLQLVESKDAGIRTLVMLDQEGEQLERI 60
Db 1 MAEDADMRNELEEMQRRADQLADESLSTRMLQLVESKDAGIRTLVMLDQEGEQLERI 60
Qy 61 BEGMDQINKDMKEAEKNLTDLGKFCGLVCPCNKLKSSDAYKKAAGNNQGVVASQPARV 120
Db 61 BEGMDQINKDMKEAEKNLTDLGKFCGLVCPCNKLKSSDAYKKAAGNNQGVVASQPARV 120
Qy 121 VDREQMAISGGFIRRTVNDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTONRQIDR 180
Db 121 VDREQMAISGGFIRRTVNDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTONRQIDR 180
Qy 181 IMEKADSNKTRIDEANORATKMLGSG 206
Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 4
US-09-949-016-10671
; Sequence 10671, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10671
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10671

Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 3
US-09-949-016-6311
; Sequence 6311, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6311
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6311

Query Match 100.0%; Score 1048; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.4e-97;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAEDADMRNELEEMQRRADQLADESLSTRMLQLVESKDAGIRTLVMLDQEGEQLERI 60
Db 1 MAEDADMRNELEEMQRRADQLADESLSTRMLQLVESKDAGIRTLVMLDQEGEQLERI 60
Qy 61 BEGMDQINKDMKEAEKNLTDLGKFCGLVCPCNKLKSSDAYKKAAGNNQGVVASQPARV 120
Db 61 BEGMDQINKDMKEAEKNLTDLGKFCGLVCPCNKLKSSDAYKKAAGNNQGVVASQPARV 120
Qy 121 VDREQMAISGGFIRRTVNDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTONRQIDR 180
Db 121 VDREQMAISGGFIRRTVNDARENEMDENLEQVSGIIGNLRHLMALDMGNEIDTONRQIDR 180
Qy 181 IMEKADSNKTRIDEANORATKMLGSG 206
Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 4
US-09-949-016-10671
; Sequence 10671, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10671
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10671

```
Query Match 100.0%; Score 1048; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 2.6e-97;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAEDADMRNELEEMQRRADQLADESLSTRMLQLVEESKDAGIRTLVMLDQEQQLERI 60
Db 14 MAEDADMRNELEEMQRRADQLADESLSTRMLQLVEESKDAGIRTLVMLDQEQQLERI 73

Qy 61 BEGMDQINKOMKEAKNLTDLGKFCGLVCPCNKLSDDAYKKAWGNQGVVASQPARV 120
Db 74 BEGMDQINKOMKEAKNLTDLGKFCGLVCPCNKLSDDAYKKAWGNQGVVASQPARV 133

Qy 121 VDREQMAISGGFRRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONRQIDR 180
Db 134 VDREQMAISGGFRRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONRQIDR 193

Qy 181 IMEKADSNKTRIDEANQRATKMLGSG 206
Db 194 IMEKADSNKTRIDEANQRATKMLGSG 219

RESULT 5
US-09-962-360B-11
; Sequence 11, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-09-962-360B-11

Query Match 55.2%; Score 578; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.7e-50;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 NKLKSSDAYKKAWGNQGVVASQPARVVDREQMAISGGFRRVTNDARENEMDENLEQ 152
Db 2 NKLKSSDAYKKAWGNQGVVASQPARVVDREQMAISGGFRRVTNDARENEMDENLEQ 61

Qy 153 VSGIIGNLRHMLDMGNEIDTONRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
Db 62 VSGIIGNLRHMLDMGNEIDTONRQIDRIMEKADSNKTRIDEANQRATKMLGSG 115

RESULT 6
US-09-962-360B-12
; Sequence 12, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
```

```
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 12
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-09-962-360B-12

Query Match 54.6%; Score 572; DB 2; Length 116;
Best Local Similarity 99.1%; Pred. No. 6.8e-50;
Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 93 NKLKSSDAYKKAWGNQGVVASQPARVVDREQMAISGGFRRVTNDARENEMDENLEQ 152
Db 2 NKLKSSDAYKKAWGNQGVVASQPARVVDREQMAISGGFRRVTNDARENEMDENLEQ 61

Qy 153 VSGIIGNLRHMLDMGNEIDTONRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
Db 62 VSGIIGNLRHMLDMGNEIDTONRQIDRIMEKADSNKTRIDEANQRATKMLGSG 115

RESULT 7
US-09-949-016-10399
; Sequence 10399, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10399
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10399

Query Match 48.9%; Score 512; DB 2; Length 158;
Best Local Similarity 53.6%; Pred. No. 1.1e-43;
Matches 104; Conservative 22; Mismatches 26; Indels 42; Gaps 1;

Qy 12 EEMORRADQLADESLSTRMLQLVEESKDAGIRTLVMLDQEQQLERI 71
Db 7 BEIQORAHQITDESLESTRILGLAIESQDAGIKITITMLDQEQQLNRIEGLDQINKDM 66

Qy 72 KEAEKNLTDLGKFCGLVCPCNKLSDDAYKKAWGNQGVVASQPARVVDREQMAISG 131
Db 67 RETEKLTLFELNKKCGLCVPCNS ----- 89

Qy 132 GFIRRVTVNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONRQIDRIMEKADSNKTR 191
Db 90 -----ITNDAREDEMEENLTQVGSILGNLKDMLNIGNEIDAQNPOIKRITDKAUTNRDR 144
```

```
Qy 192 IDEANORATKMG 205
Db 145 IDIANARAKKIDS 158

RESULT 8
US-09-513-999C-7906
; Sequence 7906, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7906
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 71
; OTHER INFORMATION: Xaa=Met or Arg
; NAME/KEY: UNSURE
; LOCATION: 72
; OTHER INFORMATION: Xaa=Glu or Gly or Lys or Arg
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 92
; OTHER INFORMATION: Xaa=Gly or Val
; US-09-513-999C-7906

Query Match 43.0%; Score 451; DB 2; Length 106;
Best Local Similarity 94.7%; Pred. No. 8.5e-38;
Matches 90; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
Db 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
Qy 61 EEGMDQINKDMKEAEKNLTDLGKFCGLVCPCNKL 95
Db 61 EEGMDQINKDXEAEKNLTDLGKFCGLVCPCXTSL 95

RESULT 9
US-09-513-999C-7907
; Sequence 7907, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7907
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 71
; OTHER INFORMATION: Xaa=Met or Arg
; NAME/KEY: UNSURE
; LOCATION: 72
; OTHER INFORMATION: Xaa=Glu or Gly or Lys or Arg
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 92
; OTHER INFORMATION: Xaa=Gly or Val
; US-09-513-999C-7906

Query Match 43.0%; Score 451; DB 2; Length 106;
Best Local Similarity 94.7%; Pred. No. 8.5e-38;
Matches 90; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
Db 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
Qy 61 EEGMDQINKDMKEAEKNLTDLGKFCGLVCPCNKL 95
Db 61 EEGMDQINKDXEAEKNLTDLGKFCGLVCPCXTSL 95

RESULT 9
US-09-513-999C-7907
; Sequence 7907, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7907
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 71
; OTHER INFORMATION: Xaa=Met or Arg
; NAME/KEY: UNSURE
; LOCATION: 72
; OTHER INFORMATION: Xaa=Glu or Gly or Lys or Arg
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 92
; OTHER INFORMATION: Xaa=Gly or Val
; US-09-513-999C-7907

Query Match 43.0%; Score 451; DB 2; Length 106;
Best Local Similarity 94.7%; Pred. No. 8.5e-38;
Matches 90; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
Db 1 MAEDADMRNELEEMORRADQADLESLESTRMLQLVEESKDAGIRTLVMLDEQGEQLERI 60
Qy 61 EEGMDQINKDMKEAEKNLTDLGKFCGLVCPCNKL 95
Db 61 EEGMDQINKDXEAEKNLTDLGKFCGLVCPCXTSL 95

RESULT 10
US-08-760-001-10
; Sequence 10, Application US/08760001
; Patent No. 5962637
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/760,001
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
```

US-08-760-001-10

Query Match 33.7%; Score 353; DB 1; Length 70;
 Best Local Similarity 100.0%; Pred. No. 3.4e-28;
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 137 VTNDARENEMDENLEQVSGIIGNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196
 DB 1 VTNDARENEMDENLEQVSGIIGNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 60
 QY 197 QRATKMLGSG 206
 DB 61 QRATKMLGSG 70

RESULT 11

US-09-015-960-10
 ; Sequence 10, Application US/09015960
 ; Patent No. 6043042
 ; GENERAL INFORMATION:
 ; APPLICANT: Shone, Clifford C.
 ; APPLICANT: Hallis, Basam
 ; APPLICANT: James, Benjamin A. F.
 ; APPLICANT: Quinn, Conrad P.
 ; TITLE OF INVENTION: TOXIN ASSAY
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 ; STREET: 1100 New York Ave., N.W., Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/015,960
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/760,001
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Esmond, Robert W.
 ; REGISTRATION NUMBER: 32,893
 ; REFERENCE/DOCKET NUMBER: 1581.0120001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2543
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 70 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-09-015-960-10

Query Match 33.7%; Score 353; DB 2; Length 70;
 Best Local Similarity 100.0%; Pred. No. 3.4e-28;
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 137 VTNDARENEMDENLEQVSGIIGNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196
 DB 1 VTNDARENEMDENLEQVSGIIGNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 60
 QY 197 QRATKMLGSG 206
 DB 61 QRATKMLGSG 70

RESULT 12

US-09-534-572-10
 ; Sequence 10, Application US/09534572
 ; Patent No. 6337386
 ; GENERAL INFORMATION:
 ; APPLICANT: Shone, Clifford C.
 ; APPLICANT: Hallis, Basam
 ; APPLICANT: James, Benjamin A. F.
 ; APPLICANT: Quinn, Conrad P.
 ; TITLE OF INVENTION: TOXIN ASSAY
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 ; STREET: 1100 New York Ave., N.W., Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/534,572
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/015,960
 ; FILING DATE: 30-JAN-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/760,001
 ; FILING DATE: 30-DEC-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB95/01279
 ; FILING DATE: 02-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Esmond, Robert W.
 ; REGISTRATION NUMBER: 32,893
 ; REFERENCE/DOCKET NUMBER: 1581.0120003
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2543
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 70 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-09-534-572-10

Query Match 33.7%; Score 353; DB 2; Length 70;
 Best Local Similarity 100.0%; Pred. No. 3.4e-28;
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 VTNDARENEMDENLEQVSGIIGNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196
 DB 1 VTNDARENEMDENLEQVSGIIGNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 60
 QY 197 QRATKMLGSG 206
 DB 61 QRATKMLGSG 70

RESULT 13

US-09-513-999C-4845
 ; Sequence 4845, Application US/09513999C
 ; Patent No. 6783961
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Duclert, A.

```
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4845
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-513-999C-4845

Query Match      29.6%; Score 310; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 6.2e-24;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAEDADMRNLEENQRRADQLADESLESTRMLQLVVEESKDAGIRTLVMLDQEQEQLERI 60
Db 1 MAEDADMRNLEENQRRADQLADESLESTRMLQLVVEESKDAGIRTLVMLDQEQEQLERI 60

Qy 61 EEGM 64
Db 61 EEGM 64

RESULT 14
US-09-621-976-7614
; Sequence 7614, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 7614
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-621-976-7614

Query Match      26.4%; Score 277; DB 2; Length 68;
Best Local Similarity 98.3%; Pred. No. 1.4e-20;
Matches 57; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAEDADMRNLEENQRRADQLADESLESTRMLQLVVEESKDAGIRTLVMLDQEQEQL 58
Db 1 MAEDADMRNLEENQRRADQLADESLESTRMLQLVVEESKDAGIRTLVMLDQEQEQLQ 58

RESULT 15
US-09-952-689-9
; Sequence 9, Application US/09952689
; Patent No. 6784341
; GENERAL INFORMATION:
; APPLICANT: Jöhal, Gurmukh S.
; APPLICANT: Multani, Dilbag
; TITLE OF INVENTION: Defense-Related Signaling Genes and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 35718/237947
; CURRENT APPLICATION NUMBER: US/09/952,689
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/232,538
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 9
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Arabidopsis
; US-09-952-689-9

Query Match      21.9%; Score 230; DB 2; Length 300;
Best Local Similarity 27.3%; Pred. No. 5.3e-15;
Matches 60; Conservative 45; Mismatches 71; Indels 44; Gaps 5;

Qy 11 LEEMQRRADQLADESLESTRMLQLVVEESKDAGIRTLVMLDQEQEQLERIEEGMDQINKD 70
Db 98 VQELGVAVYKABETTKSVQGLKVAEDIRSDATRTLVMLHDQEQQITRTHKAVEIDHD 157

Qy 71 MKEAEKNLTDLGKFCGLCVPCNKLKSSDAYKAWGNQ-----DGVVASQ---PARVVDE 123
Db 158 LSRGEXLLGSLG-----GMFSKTWPKKTRPINGPVVTRDDSPTRRVNH 201

Qy 124 -----REQMAISGGFTRRRVNTNDARENEMDENLEQVSGIIGNLRHMA 164
Db 202 LEKREKLGINSAPRGQSRTRPELPESADAYQRV--EMEKAQDDGLSDLSLILGELKNMA 259

Qy 165 LDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRAATKMLG 204
Db 260 VDMGSEIEKQNGKGLDHDVDDELNFRVQSQNQRRELLG 299

Search completed: April 3, 2006, 15:18:00
Job time : 55.8226 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:23:07 ; Search time 2.19355 Seconds

(without alignments)
235.925 Million cell updates/sec

Title: US-09-942-098-2_COPY_187_203

Perfect score: 83

Sequence: 1 SNKTRIDEANQRATKML 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB.pdp.*
- 2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pdp.*
- 3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pdp.*
- 4: /SIDSS/ptodata/1/pubpaa/PTCT_NEW_PUB.pdp.*
- 5: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB.pdp.*
- 6: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pdp.*
- 7: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pdp.*
- 8: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	83	100.0	17	6	US-10-980-346B-6	Sequence 6, Appl
2	83	100.0	17	6	US-10-980-346B-37	Sequence 37, Appl
3	83	100.0	17	6	US-10-947-071-33	Sequence 33, Appl
4	83	100.0	17	6	US-10-948-097-33	Sequence 33, Appl
5	83	100.0	18	6	US-10-947-071-35	Sequence 35, Appl
6	83	100.0	18	6	US-10-948-097-35	Sequence 35, Appl
7	83	100.0	33	6	US-10-947-071-36	Sequence 36, Appl
8	83	100.0	33	6	US-10-947-071-40	Sequence 40, Appl
9	83	100.0	33	6	US-10-947-071-41	Sequence 41, Appl
10	83	100.0	33	6	US-10-948-097-36	Sequence 36, Appl
11	83	100.0	33	6	US-10-948-097-40	Sequence 40, Appl
12	83	100.0	33	6	US-10-948-097-41	Sequence 41, Appl
13	83	100.0	116	7	US-11-195-098-11	Sequence 11, Appl
14	83	100.0	203	6	US-10-947-071-4	Sequence 4, Appl
15	83	100.0	203	6	US-10-948-097-4	Sequence 4, Appl
16	83	100.0	206	6	US-10-947-071-1	Sequence 1, Appl
17	83	100.0	206	6	US-10-947-071-2	Sequence 2, Appl
18	83	100.0	206	6	US-10-948-097-1	Sequence 1, Appl
19	83	100.0	206	6	US-10-948-097-2	Sequence 2, Appl
20	83	100.0	206	7	US-11-169-041-225	Sequence 225, App
21	83	100.0	334	6	US-10-947-071-20	Sequence 20, Appl
22	83	100.0	334	6	US-10-948-097-20	Sequence 20, Appl
23	80	96.4	17	6	US-10-947-071-61	Sequence 61, Appl
24	80	96.4	17	6	US-10-948-097-61	Sequence 61, Appl
25	79	95.2	16	6	US-10-947-071-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-10-980-346B-6

; Sequence 6, Application US/10980346B

; Publication No. US20060024763A1

; GENERAL INFORMATION:

; APPLICANT: Los Alamos National Laboratory

; APPLICANT: Schmidt, Jurgen G., et al.

; TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation

; TITLE OF INVENTION: of Botulinum Neurotoxins

; FILE REFERENCE: S-102,313

; CURRENT APPLICATION NUMBER: US/10/980,346B

; CURRENT FILING DATE: 2004-11-03

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6

; LENGTH: 17

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum

; OTHER INFORMATION: Neurotoxin (BoNT)

US-10-980-346B-6

Query Match 100.0%; Score 83; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 8.1e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17

Db 1 SNKTRIDEANQRATKML 17

RESULT 2

US-10-980-346B-37

; Sequence 37, Application US/10980346B

; Publication No. US20060024763A1

; GENERAL INFORMATION:

; APPLICANT: Los Alamos National Laboratory

; APPLICANT: Schmidt, Jurgen G., et al.

; TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation

; TITLE OF INVENTION: of Botulinum Neurotoxins

; FILE REFERENCE: S-102,313

; CURRENT APPLICATION NUMBER: US/10/980,346B

; CURRENT FILING DATE: 2004-11-03

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 37

; LENGTH: 17

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum
; OTHER INFORMATION: Neurotoxin (BoNT)
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(17)
; OTHER INFORMATION: amide bound at one end of the peptide
US-10-980-346B-37

Query Match      100.0%; Score 83; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 1 SNKTRIDEANQRATKML 17

RESULT 3
US-10-947-071-33
; Sequence 33, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-33

Query Match      100.0%; Score 83; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 1 SNKTRIDEANQRATKML 17

RESULT 4
US-10-948-097-33
; Sequence 33, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-33

Query Match      100.0%; Score 83; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 1 SNKTRIDEANQRATKML 17

RESULT 5
US-10-947-071-35
; Sequence 35, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-35

Query Match      100.0%; Score 83; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18

RESULT 6
US-10-948-097-35
; Sequence 35, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-35

Query Match      100.0%; Score 83; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18
```

```
US-10-948-097-33

Query Match      100.0%; Score 83; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 1 SNKTRIDEANQRATKML 17

RESULT 5
US-10-947-071-35
; Sequence 35, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-35

Query Match      100.0%; Score 83; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18

RESULT 6
US-10-948-097-35
; Sequence 35, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-35

Query Match      100.0%; Score 83; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18
```

```

; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
; ORGANISM: Carassius auratus
US-10-947-071-41

Query Match      100.0%; Score 83; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKML 17
Db      14 SNKTRIDEANQRATKML 30

RESULT 10
US-10-948-097-36
; Sequence 36, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
; ORGANISM: Mus musculus
US-10-948-097-36

Query Match      100.0%; Score 83; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKML 17
Db      14 SNKTRIDEANQRATKML 30

RESULT 11
US-10-948-097-40
; Sequence 40, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
; ORGANISM: Carassius auratus
US-10-947-071-40

Query Match      100.0%; Score 83; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKML 17
Db      14 SNKTRIDEANQRATKML 30

RESULT 9
US-10-947-071-41
; Sequence 41, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
; ORGANISM: Mus musculus
US-10-947-071-36

Query Match      100.0%; Score 83; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKML 17
Db      14 SNKTRIDEANQRATKML 30

RESULT 8
US-10-947-071-40
; Sequence 40, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
; ORGANISM: Carassius auratus
US-10-947-071-40

Query Match      100.0%; Score 83; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKML 17
Db      14 SNKTRIDEANQRATKML 30

RESULT 7
US-10-947-071-36
; Sequence 36, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
; ORGANISM: Mus musculus
US-10-947-071-36
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-40

Query Match          100.0%; Score 83; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
   |||||
Db 14 SNKTRIDEANQRATKML 30

RESULT 12
US-10-948-097-41
; Sequence 41, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-41

Query Match          100.0%; Score 83; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
   |||||
Db 14 SNKTRIDEANQRATKML 30

RESULT 13
US-11-195-098-11
; Sequence 11, Application US/11195098
; Publication No. US20050287622A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/11/195,098
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/802,574
; PRIOR FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 09/962,360
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-11-195-098-11

Query Match          100.0%; Score 83; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
   |||||
Db 96 SNKTRIDEANQRATKML 112

RESULT 14
US-10-947-071-4
; Sequence 4, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-4

Query Match          100.0%; Score 83; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
   |||||
Db 184 SNKTRIDEANQRATKML 200

RESULT 15
US-10-948-097-4
; Sequence 4, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-4

Query Match          100.0%; Score 83; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
   |||||
Db 184 SNKTRIDEANQRATKML 200
```

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQATKML 17

Db 184 SNKTRIDEANQATKML 200

Search completed: April 3, 2006, 15:27:30
Job time : 2.19355 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:21:47 ; Search time 16.0403 Seconds
(without alignments)
442.828 Million cell updates/sec

Title: US-09-942-098-2_COPY_187_203

Perfect score: 83
Sequence: 1 SNKTRIDEANQRATKML 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main.*

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	17	3	US-09-942-024-30
2	83	100.0	17	3	US-09-942-098-30
3	83	100.0	17	4	US-10-011-588-2
4	83	100.0	17	4	US-10-261-161-52
5	83	100.0	17	4	US-10-261-161-68
6	83	100.0	17	5	US-10-917-844-30
7	83	100.0	18	3	US-09-942-024-32
8	83	100.0	18	3	US-09-942-098-32
9	83	100.0	18	4	US-10-261-161-54
10	83	100.0	18	5	US-10-917-844-32
11	83	100.0	19	4	US-10-705-857-6
12	83	100.0	21	3	US-09-942-024-89
13	83	100.0	21	3	US-09-942-098-89
14	83	100.0	23	3	US-09-942-024-88
15	83	100.0	23	3	US-09-942-098-88
16	83	100.0	24	3	US-09-942-024-90
17	83	100.0	24	3	US-09-942-098-90
18	83	100.0	33	3	US-09-942-024-33
19	83	100.0	33	3	US-09-942-024-37
20	83	100.0	33	3	US-09-942-024-38
21	83	100.0	33	3	US-09-942-098-33
22	83	100.0	33	3	US-09-942-098-37
23	83	100.0	33	3	US-09-942-098-38
24	83	100.0	33	4	US-10-261-161-55
25	83	100.0	33	4	US-10-261-161-59
26	83	100.0	33	4	US-10-261-161-60
27	83	100.0	33	5	US-10-917-844-33

28	83	100.0	33	5	US-10-917-844-37	Sequence 37, Appl
29	83	100.0	33	5	US-10-917-844-38	Sequence 38, Appl
30	83	100.0	86	4	US-10-705-857-4	Sequence 4, Appl
31	83	100.0	114	5	US-10-917-844-112	Sequence 112, App
32	83	100.0	116	3	US-09-962-360B-11	Sequence 11, Appl
33	83	100.0	116	4	US-10-802-574-11	Sequence 11, Appl
34	83	100.0	203	3	US-09-942-024-14	Sequence 14, Appl
35	83	100.0	203	3	US-09-942-098-14	Sequence 14, Appl
36	83	100.0	203	4	US-10-261-161-7	Sequence 7, Appl
37	83	100.0	203	5	US-10-917-844-14	Sequence 14, Appl
38	83	100.0	206	3	US-09-942-024-2	Sequence 2, Appl
39	83	100.0	206	3	US-09-942-024-12	Sequence 12, Appl
40	83	100.0	206	3	US-09-942-098-2	Sequence 2, Appl
41	83	100.0	206	3	US-09-942-098-7	Sequence 7, Appl
42	83	100.0	206	3	US-09-942-098-12	Sequence 12, Appl
43	83	100.0	206	4	US-10-261-161-4	Sequence 4, Appl
44	83	100.0	206	4	US-10-261-161-5	Sequence 5, Appl
45	83	100.0	206	4	US-10-261-161-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-942-024-30
; Sequence 30, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-30

Query Match 100.0%; Score 83; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
| | | | | | | | | | | | | | | | | |
Db 1 SNKTRIDEANQRATKML 17

RESULT 2
US-09-942-098-30
; Sequence 30, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-30

Query Match 100.0%; Score 83; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
|||||
Db 1 SNKTRIDEANQRATKML 17

RESULT 3
US-10-011-588-2
; Sequence 2, Application US/10011588
; Publication No. US20020169727A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Leonard
; APPLICANT: Jensen, Melody
; TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS AND LIGHT CHAIN FUSION PROTEINS FOR USE IN
; TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY
; FILE REFERENCE: A34796 067252.0113
; CURRENT APPLICATION NUMBER: US/10/011,588
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 09/910,186
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/611,419
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 60/246,744
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 60/311,966
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (O)...(O)
; OTHER INFORMATION: Residues 187-203 of SNAP-25
US-10-011-588-2

Query Match 100.0%; Score 83; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
|||||
Db 1 SNKTRIDEANQRATKML 17

RESULT 4
US-10-261-161-52
; Sequence 52, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-52

Query Match 100.0%; Score 83; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
|||||
Db 1 SNKTRIDEANQRATKML 17

RESULT 5
US-10-261-161-68
; Sequence 68, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-261-161-68

Query Match 100.0%; Score 83; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
|||||
Db 1 SNKTRIDEANQRATKML 17

RESULT 6
US-10-917-844-30
; Sequence 30, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
; APPLICANT: Aoki, Kei R.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
; FILE REFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917,844
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-844-30

Query Match 100.0%; Score 83; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
|||||
Db 1 SNKTRIDEANQRATKML 17

```
RESULT 7
US-09-942-024-32
; Sequence 32, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-32

Query Match      100.0%; Score 83; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18

RESULT 8
US-09-942-098-32
; Sequence 32, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-32

Query Match      100.0%; Score 83; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18

RESULT 9
US-10-261-161-54
; Sequence 54, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
```

```
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-54

Query Match      100.0%; Score 83; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18

RESULT 10
US-10-917-844-32
; Sequence 32, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
; APPLICANT: Aoki, Kei R.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
; FILE REFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917,844
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-844-32

Query Match      100.0%; Score 83; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18

RESULT 11
US-10-705-857-6
; Sequence 6, Application US/10705857
; Publication No. US20040147443A1
; GENERAL INFORMATION:
; APPLICANT: RENAULT, BEATRICE
; TITLE OF INVENTION: USE OF A COMBINATION OF COMPONENTS WITH AN INHIBITORY
; TITLE OF INVENTION: SYNERGISTIC EFFECT ON CALCIUM CHANNELS TO PREVENT OR
; TITLE OF INVENTION: TREAT WRINKLES AND FINE LINES
; FILE REFERENCE: 05725.1275
; CURRENT APPLICATION NUMBER: US/10/705,857
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/427,575
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: FR 0214183
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
```

```
; OTHER INFORMATION: peptide
US-10-705-857-6

Query Match      100.0%; Score 83; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 3 SNKTRIDEANQRATKML 19

RESULT 12
US-09-942-024-89
; Sequence 89, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 21
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-89

Query Match      100.0%; Score 83; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 4 SNKTRIDEANQRATKML 20

RESULT 13
US-09-942-024-89
; Sequence 89, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 21
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-89

Query Match      100.0%; Score 83; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 4 SNKTRIDEANQRATKML 20

RESULT 14
US-09-942-024-88
; Sequence 88, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 23
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-88

Query Match      100.0%; Score 83; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 3 SNKTRIDEANQRATKML 19

RESULT 15
US-09-942-098-88
; Sequence 88, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
```

```

; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 23
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-88

```

```

Query Match      100.0%; Score 83; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SNKTRIDEANQRTKML 17
        |||||
Db      3 SNKTRIDEANQRTKML 19

```

```

Search completed: April 3, 2006, 15:26:52
Job time : 16.0403 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:16:44 ; Search time 4.52419 Seconds
(without alignments)

310.660 Million cell updates/sec

Title: US-09-942-098-2_COPY_187_203

Perfect score: 83

Sequence: 1 SNKTRIDEANQRATKML 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 40 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCRU5_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	17	1	US-08-743-894B-1
2	83	100.0	17	1	US-08-743-894B-37
3	83	100.0	20	2	US-08-819-286-9
4	83	100.0	26	2	US-08-819-286-8
5	83	100.0	37	2	US-08-813-286-4
6	83	100.0	70	1	US-08-760-001-10
7	83	100.0	70	2	US-09-015-960-10
8	83	100.0	70	2	US-09-534-572-10
9	83	100.0	116	2	US-09-962-360B-11
10	83	100.0	206	1	US-08-393-985-18
11	83	100.0	206	2	US-08-813-286-1
12	83	100.0	206	2	US-09-949-016-6311
13	83	100.0	219	2	US-09-949-016-10671
14	80	96.4	17	1	US-08-743-894B-18
15	80	96.4	17	1	US-08-743-894B-43
16	79	95.2	16	1	US-08-743-894B-49
17	79	95.2	17	1	US-08-743-894B-27
18	79	95.2	17	1	US-08-743-894B-30
19	79	95.2	17	1	US-08-743-894B-32
20	79	95.2	17	1	US-08-743-894B-39
21	78	94.0	17	1	US-08-743-894B-19
22	78	94.0	17	1	US-08-743-894B-25
23	78	94.0	17	1	US-08-743-894B-29
24	78	94.0	17	1	US-08-743-894B-42
25	78	94.0	17	1	US-08-743-894B-50
26	77	92.8	17	1	US-08-743-894B-2
27	77	92.8	17	1	US-08-743-894B-20

ALIGNMENTS

RESULT 1

US-08-743-894B-1
; Sequence 1, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:

APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn: John Moran-Patent Atty
STREET: USA MEMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743.894B
FILING DATE: No. 5965699member 6, 1996

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-743-894B-1

Query Match 100.0%; Score 83; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17

DB 1 SNKTRIDEANQRATKML 17

Sequence 24, Appl
Sequence 26, Appl
Sequence 28, Appl
Sequence 31, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 36, Appl
Sequence 44, Appl
Sequence 46, Appl
Sequence 48, Appl
Sequence 38, Appl
Sequence 3, Appli

28 77 92.8 17 1 US-08-743-894B-24
29 77 92.8 17 1 US-08-743-894B-26
30 77 92.8 17 1 US-08-743-894B-28
31 77 92.8 17 1 US-08-743-894B-31
32 77 92.8 17 1 US-08-743-894B-33
33 77 92.8 17 1 US-08-743-894B-34
34 77 92.8 17 1 US-08-743-894B-36
35 77 92.8 17 1 US-08-743-894B-44
36 77 92.8 17 1 US-08-743-894B-45
37 77 92.8 17 1 US-08-743-894B-46
38 77 92.8 24 2 US-09-962-360B-8
39 77 92.8 116 2 US-09-962-360B-12
40 75 90.4 17 1 US-08-743-894B-21
41 75 90.4 17 1 US-08-743-894B-35
42 75 90.4 17 1 US-08-743-894B-47
43 75 90.4 17 1 US-08-743-894B-48
44 74 89.2 15 1 US-08-743-894B-38
45 74 89.2 17 1 US-08-743-894B-3

TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-819-286-8

Query Match 100.0%; Score 83; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRAKML 17
Db 7 SNKTRIDEANQRAKML 23

RESULT 5
US-08-819-286-4
Sequence 4, Application US/08819286
Patent No. 6169074

GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-819-286-4

Query Match 100.0%; Score 83; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRAKML 17
Db 18 SNKTRIDEANQRAKML 34

RESULT 6
US-08-760-001-10
Sequence 10, Application US/08760001
Patent No. 5962637
GENERAL INFORMATION:

APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Basam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,001
FILING DATE: Herewith
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-760-001-10

Query Match 100.0%; Score 83; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRAKML 17
Db 51 SNKTRIDEANQRAKML 67

RESULT 7
US-09-015-960-10
Sequence 10, Application US/09015960
Patent No. 6043042

GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Basam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,960
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-015-960-10

Query Match 100.0%; Score 83; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKML 17
Db 51 SNKTRIDEANORATKML 67

RESULT 8
US-09-534-572-10
; Sequence 10, Application US/09534572
; Patent No. 6337386
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,572
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,960
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE: 30-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120003
; TELECOMMUNICATION INFORMATION:

;
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-534-572-10

Query Match 100.0%; Score 83; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKML 17
Db 51 SNKTRIDEANORATKML 67

RESULT 9
US-09-962-360B-11
; Sequence 11, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoreseceinyl-cysteine
; US-09-962-360B-11

Query Match 100.0%; Score 83; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKML 17
Db 96 SNKTRIDEANORATKML 112

RESULT 10
US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Scheller, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA

```
;
;
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-393-985-18

Query Match 100.0%; Score 83; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 187 SNKTRIDEANQRATKML 203

RESULT 11
US-08-819-286-1
; Sequence 1, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid

;
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-1

Query Match 100.0%; Score 83; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 187 SNKTRIDEANQRATKML 203

RESULT 12
US-09-949-016-6311
; Sequence 6311, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6311
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6311

Query Match 100.0%; Score 83; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 187 SNKTRIDEANQRATKML 203

RESULT 13
US-09-949-016-10671
; Sequence 10671, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10671
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10671
```

```
Query Match          100.0%; Score 83; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 9.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKML 17
       |||||
Db      200 SNKTRIDEANQRATKML 216

RESULT 14
US-08-743-894B-18
; Sequence 18, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
US-08-743-894B-18

Query Match          96.4%; Score 80; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.7e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKML 17
       |||||
Db      1 SNKTRIDEANQRATKML 17

Search completed: April 3, 2006, 15:18:00
Job time : 4.52419 secs

RESULT 15
US-08-743-894B-43
; Sequence 43, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
```

```
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
US-08-743-894B-43

Query Match          96.4%; Score 80; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.7e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKML 17
       |||||
Db      1 SNKTRIDEANQRATKML 17

Search completed: April 3, 2006, 15:18:00
Job time : 4.52419 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:49:32 ; Search time 6.38532 Seconds
(without alignments)
57.210 Million cell updates/sec

Title: US-09-942-098-2_COPY_191_202

Perfect score: 59

Sequence: 1 RIDEANQRATKM 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pap.*
2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pap.*
3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pap.*
4: /SIDSS/ptodata/1/pubpaa/PTCT_NEW PUB.pap.*
5: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pap.*
6: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pap.*
7: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pap.*
8: /SIDSS/ptodata/1/pubpaa/US60_NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	59	100.0	13	US-10-947-071-30
2	59	100.0	13	US-10-948-097-30
3	59	100.0	16	US-10-947-071-32
4	59	100.0	16	US-10-948-097-32
5	59	100.0	17	US-10-980-346B-6
6	59	100.0	17	US-10-980-346B-37
7	59	100.0	17	US-10-947-071-33
8	59	100.0	17	US-10-947-071-34
9	59	100.0	17	US-10-948-097-33
10	59	100.0	17	US-10-948-097-34
11	59	100.0	18	US-10-947-071-35
12	59	100.0	18	US-10-948-097-35
13	59	100.0	33	US-10-947-071-36
14	59	100.0	33	US-10-947-071-40
15	59	100.0	33	US-10-947-071-41
16	59	100.0	33	US-10-948-097-36
17	59	100.0	33	US-10-948-097-40
18	59	100.0	33	US-10-948-097-41
19	59	100.0	116	US-11-195-098-11
20	59	100.0	203	US-10-947-071-4
21	59	100.0	203	US-10-948-097-4
22	59	100.0	206	US-10-947-071-1
23	59	100.0	206	US-10-947-071-2
24	59	100.0	206	US-10-948-097-1
25	59	100.0	206	US-10-948-097-2

26	59	100.0	206	7	US-11-169-041-225	Sequence 225, App
27	59	100.0	334	6	US-10-947-071-20	Sequence 20, Appl
28	59	100.0	334	6	US-10-948-097-20	Sequence 20, Appl
29	56	94.9	17	6	US-10-980-346B-38	Sequence 38, Appl
30	56	94.9	17	6	US-10-947-071-61	Sequence 61, Appl
31	56	94.9	17	6	US-10-948-097-61	Sequence 61, Appl
32	56	94.9	22	6	US-10-980-346B-1	Sequence 1, Appl
33	56	94.9	24	7	US-11-195-098-8	Sequence 8, Appl
34	55	93.2	17	6	US-10-947-071-53	Sequence 53, Appl
35	55	93.2	17	6	US-10-947-071-55	Sequence 55, Appl
36	55	93.2	17	6	US-10-947-071-60	Sequence 60, Appl
37	55	93.2	17	6	US-10-948-097-53	Sequence 53, Appl
38	55	93.2	17	6	US-10-948-097-55	Sequence 55, Appl
39	55	93.2	17	6	US-10-948-097-60	Sequence 60, Appl
40	54	91.5	15	6	US-10-947-071-31	Sequence 31, Appl
41	54	91.5	15	6	US-10-948-097-31	Sequence 31, Appl
42	54	91.5	17	6	US-10-947-071-50	Sequence 50, Appl
43	54	91.5	17	6	US-10-947-071-51	Sequence 51, Appl
44	54	91.5	17	6	US-10-947-071-54	Sequence 54, Appl
45	54	91.5	17	6	US-10-947-071-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-10-947-071-30
; Sequence 30, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947.071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-30

Query Match 100.0%; Score 59; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.7e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIDEANQRATKM 12
DB 2 RIDEANQRATKM 13

RESULT 2
US-10-948-097-30
; Sequence 30, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-30

Query Match 100.0%; Score 59; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.7e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
Db 2 RIDEANORATKM 13
|||||

RESULT 3
US-10-947-071-32
; Sequence 32, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-32

Query Match 100.0%; Score 59; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
Db 5 RIDEANORATKM 16
|||||

RESULT 4
US-10-948-097-32
; Sequence 32, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-32

Query Match 100.0%; Score 59; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RIDEANORATKM 12
Db 5 RIDEANORATKM 16
|||||

RESULT 5
US-10-980-346B-6
; Sequence 6, Application US/10980346B
; Publication No. US20060024763A1
; GENERAL INFORMATION:
; APPLICANT: Los Alamos National Laboratory
; APPLICANT: Schmidt, Jurgen G., et al.
; TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
; FILE REFERENCE: S-102,313
; CURRENT APPLICATION NUMBER: US/10/980,346B
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum
; OTHER INFORMATION: Neurotoxin (BoNT)
US-10-980-346B-6

Query Match 100.0%; Score 59; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
Db 5 RIDEANORATKM 16
|||||

RESULT 6
US-10-980-346B-37
; Sequence 37, Application US/10980346B
; Publication No. US20060024763A1
; GENERAL INFORMATION:
; APPLICANT: Los Alamos National Laboratory
; APPLICANT: Schmidt, Jurgen G., et al.
; TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
; FILE REFERENCE: S-102,313
; CURRENT APPLICATION NUMBER: US/10/980,346B
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 37
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum
; OTHER INFORMATION: Neurotoxin (BoNT)
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(17)
; OTHER INFORMATION: amide bound at one end of the peptide
US-10-980-346B-37

Query Match 100.0%; Score 59; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
Db 5 RIDEANORATKM 16
|||||

```

RESULT 7
US-10-947-071-33
; Sequence 33, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-33

```

```

Query Match 100.0%; Score 59; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RIDEANORATKM 12
Db 5 RIDEANORATKM 16

```

```

RESULT 8
US-10-947-071-34
; Sequence 34, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-34

```

```

Query Match 100.0%; Score 59; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RIDEANORATKM 12
Db 6 RIDEANORATKM 17

```

```

RESULT 9
US-10-948-097-33
; Sequence 33, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.

```

```

; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-33

```

```

Query Match 100.0%; Score 59; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RIDEANORATKM 12
Db 5 RIDEANORATKM 16

```

```

RESULT 10
US-10-948-097-34
; Sequence 34, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-34

```

```

Query Match 100.0%; Score 59; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 RIDEANORATKM 12
Db 6 RIDEANORATKM 17

```

```

RESULT 11
US-10-947-071-35
; Sequence 35, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101

```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-35

Query Match      100.0%; Score 59; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
Db 6 RIDEANORATKM 17

RESULT 12
US-10-948-097-35
; Sequence 35, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-35

Query Match      100.0%; Score 59; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
Db 6 RIDEANORATKM 17

RESULT 13
US-10-947-071-36
; Sequence 36, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-947-071-36

Query Match      100.0%; Score 59; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
Db 6 RIDEANORATKM 17

RESULT 14
US-10-947-071-40
; Sequence 40, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-40

Query Match      100.0%; Score 59; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
Db 18 RIDEANORATKM 29

RESULT 15
US-10-947-071-41
; Sequence 41, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-41

Query Match      100.0%; Score 59; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
Db 18 RIDEANORATKM 29

Search completed: April 3, 2006, 15:58:09
Job time : 6.38532 secs
```

us-09-942-098-2_copy_191_202.rapbn

Mon Apr 3 16:29:15 2006

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocollaboration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:46:49 ; Search time 51.633 Seconds
(without alignments)
97.107 Million cell updates/sec

Title: US-09-942-098-2_COPY_191_202

Perfect score: 59

Sequence: 1 RIDEANQRATKM 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	13	3	US-09-942-024-27
2	59	100.0	13	3	US-09-942-098-27
3	59	100.0	13	4	US-10-261-161-49
4	59	100.0	13	5	US-10-917-844-27
5	59	100.0	16	3	US-09-942-024-29
6	59	100.0	16	3	US-09-942-024-91
7	59	100.0	16	3	US-09-942-024-94
8	59	100.0	16	3	US-09-942-098-29
9	59	100.0	16	3	US-09-942-098-91
10	59	100.0	16	3	US-09-942-098-94
11	59	100.0	16	4	US-10-261-161-51
12	59	100.0	16	4	US-10-261-161-67
13	59	100.0	16	5	US-10-917-844-29
14	59	100.0	17	3	US-09-942-024-30
15	59	100.0	17	3	US-09-942-024-31
16	59	100.0	17	3	US-09-942-098-30
17	59	100.0	17	3	US-09-942-098-31
18	59	100.0	17	4	US-10-011-588-2
19	59	100.0	17	4	US-10-261-161-52
20	59	100.0	17	4	US-10-261-161-53
21	59	100.0	17	4	US-10-261-161-68
22	59	100.0	17	5	US-10-917-844-30
23	59	100.0	17	5	US-10-917-844-31
24	59	100.0	18	3	US-09-942-024-32
25	59	100.0	18	3	US-09-942-098-32
26	59	100.0	18	4	US-10-261-161-54
27	59	100.0	18	5	US-10-917-844-32

28	59	100.0	19	3	US-09-942-024-85	Sequence 85, Appl
29	59	100.0	19	3	US-09-942-024-92	Sequence 92, Appl
30	59	100.0	19	3	US-09-942-024-95	Sequence 95, Appl
31	59	100.0	19	3	US-09-942-098-85	Sequence 85, Appl
32	59	100.0	19	3	US-09-942-098-92	Sequence 92, Appl
33	59	100.0	19	3	US-09-942-098-95	Sequence 95, Appl
34	59	100.0	19	4	US-10-705-857-6	Sequence 6, Appl
35	59	100.0	21	3	US-09-942-024-89	Sequence 89, Appl
36	59	100.0	21	3	US-09-942-098-89	Sequence 89, Appl
37	59	100.0	22	3	US-09-942-024-93	Sequence 93, Appl
38	59	100.0	22	3	US-09-942-098-93	Sequence 93, Appl
39	59	100.0	22	3	US-09-942-024-88	Sequence 88, Appl
40	59	100.0	23	3	US-09-942-098-88	Sequence 88, Appl
41	59	100.0	24	3	US-09-942-024-90	Sequence 90, Appl
42	59	100.0	24	3	US-09-942-098-90	Sequence 90, Appl
43	59	100.0	33	3	US-09-942-024-33	Sequence 33, Appl
44	59	100.0	33	3	US-09-942-024-37	Sequence 37, Appl
45	59	100.0	33	3	US-09-942-024-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-09-942-024-27
; Sequence 27, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-27

Query Match 100.0%; Score 59; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANQRATKM 12
| | | | | | | | | |
Db 2 RIDEANQRATKM 13

RESULT 2
US-09-942-098-27
; Sequence 27, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-27

```
Query Match      100.0%; Score 59; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RIDEANQRATKM 12
      |||||||
Db      2 RIDEANQRATKM 13

RESULT 3
US-10-261-161-49
; Sequence 49, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261.161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-49

Query Match      100.0%; Score 59; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RIDEANQRATKM 12
      |||||||
Db      2 RIDEANQRATKM 13

RESULT 4
US-10-917-844-27
; Sequence 27, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
; APPLICANT: Aoki, Kei R.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
; FILE REFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917.844
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-844-27

Query Match      100.0%; Score 59; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RIDEANQRATKM 12
      |||||||
Db      2 RIDEANQRATKM 13

RESULT 5
US-09-942-098-2_copy_191_202.rapbm
```

```
US-09-942-024-29
; Sequence 29, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942.024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-29

Query Match      100.0%; Score 59; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RIDEANQRATKM 12
      |||||||
Db      5 RIDEANQRATKM 16

RESULT 6
US-09-942-024-91
; Sequence 91, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942.024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa-fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 16
; OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-91

Query Match      100.0%; Score 59; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RIDEANQRATKM 12
      |||||||
Db      3 RIDEANQRATKM 14

RESULT 7
US-09-942-024-94
; Sequence 94, Application US/09942024
```

```
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa-DABCVL modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 16
; OTHER INFORMATION: Xaa=BDANS modified glutamate
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
; US-09-942-024-94
```

```
Query Match 100.0%; Score 59; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RIDEANQRATKM 12
Db 3 RIDEANQRATKM 14
|||||
```

```
RESULT 8
US-09-942-098-29
; Sequence 29, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-942-098-29
```

```
Query Match 100.0%; Score 59; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RIDEANQRATKM 12
Db 5 RIDEANQRATKM 16
|||||
```

```
RESULT 9
US-09-942-098-91
; Sequence 91, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa-fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 16
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
; US-09-942-098-91
```

```
Query Match 100.0%; Score 59; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RIDEANQRATKM 12
Db 3 RIDEANQRATKM 14
|||||
```

```
RESULT 10
US-09-942-098-94
; Sequence 94, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa-DABCVL modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 16
; OTHER INFORMATION: Xaa=BDANS modified glutamate
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
; US-09-942-098-94
```

```
Query Match 100.0%; Score 59; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RIDEANQRATKM 12
```

```
|||||
Db      3 RIDEANORATKM 14

RESULT 11
US-10-261-161-51
; Sequence 51, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-51

Query Match      100.0%; Score 59; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RIDEANORATKM 12
Db      5 RIDEANORATKM 16

RESULT 12
US-10-261-161-67
; Sequence 67, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-261-161-67

Query Match      100.0%; Score 59; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RIDEANORATKM 12
Db      5 RIDEANORATKM 16

RESULT 13
US-10-917-844-29
; Sequence 29, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
```

```
; APPLICANT: Aoki, Kei R.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; FILE REFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917,844
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-844-29

Query Match      100.0%; Score 59; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RIDEANORATKM 12
Db      5 RIDEANORATKM 16

RESULT 14
US-09-942-024-30
; Sequence 30, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: FRET Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-30

Query Match      100.0%; Score 59; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RIDEANORATKM 12
Db      5 RIDEANORATKM 16

RESULT 15
US-09-942-024-31
; Sequence 31, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: FRET Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
```

Mon Apr 3 16:29:15 2006

```
! ORGANISM: Homo sapiens
US-09-942-024-31
Query Match      100.0%; Score 59; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RIDEANORATKM 12
      |||||
Db      6 RIDEANORATKM 17

Search completed: April 3, 2006, 15:57:05
Job time : 51.633 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:31:39 ; Search time 9.57798 Seconds
(without alignments)
103.582 Million cell updates/sec

Title: US-09-942-098-2_COPY_191_202

Perfect score: 59

Sequence: 1 RIDEANQRATKM 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5 COMB.pdp.*

2: /cgn2_6/ptodata/1/iaa/6 COMB.pdp.*

3: /cgn2_6/ptodata/1/iaa/H COMB.pdp.*

4: /cgn2_6/ptodata/1/iaa/PCRTUS COMB.pdp.*

5: /cgn2_6/ptodata/1/iaa/RE COMB.pdp.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	13	2 US-09-976-535A-1	Sequence 1, Appli
2	59	100.0	16	1 US-08-743-894B-49	Sequence 49, Appl
3	59	100.0	17	1 US-08-743-894B-1	Sequence 1, Appli
4	59	100.0	17	1 US-08-743-894B-19	Sequence 19, Appl
5	59	100.0	17	1 US-08-743-894B-37	Sequence 37, Appl
6	59	100.0	20	2 US-08-819-286-9	Sequence 9, Appli
7	59	100.0	26	2 US-08-819-286-8	Sequence 8, Appli
8	59	100.0	37	2 US-08-819-286-4	Sequence 4, Appli
9	59	100.0	70	1 US-08-760-001-10	Sequence 10, Appl
10	59	100.0	70	2 US-09-015-960-10	Sequence 10, Appl
11	59	100.0	70	2 US-09-534-572-10	Sequence 10, Appl
12	59	100.0	116	2 US-09-962-360B-11	Sequence 11, Appl
13	59	100.0	206	1 US-08-393-985-18	Sequence 18, Appl
14	59	100.0	206	2 US-08-819-286-1	Sequence 1, Appli
15	59	100.0	206	2 US-09-949-016-6311	Sequence 6311, Ap
16	59	100.0	219	2 US-09-949-016-10671	Sequence 10671, A
17	56	94.9	12	1 US-08-743-894B-17	Sequence 17, Appl
18	56	94.9	13	1 US-08-743-894B-16	Sequence 16, Appl
19	56	94.9	14	2 US-09-976-535A-2	Sequence 2, Appli
20	56	94.9	16	1 US-08-743-894B-7	Sequence 7, Appli
21	56	94.9	16	1 US-08-743-894B-51	Sequence 51, Appl
22	56	94.9	17	1 US-08-743-894B-2	Sequence 2, Appli
23	56	94.9	17	1 US-08-743-894B-4	Sequence 4, Appli
24	56	94.9	17	1 US-08-743-894B-18	Sequence 18, Appl
25	56	94.9	17	1 US-08-743-894B-21	Sequence 21, Appl
26	56	94.9	17	1 US-08-743-894B-23	Sequence 23, Appl
27	56	94.9	17	1 US-08-743-894B-43	Sequence 43, Appl

Sequence 8, Appli
Sequence 27, Appl
Sequence 30, Appl
Sequence 32, Appl
Sequence 39, Appl
Sequence 41, Appl
Sequence 13, Appl
Sequence 38, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 36, Appl
Sequence 42, Appl
Sequence 50, Appl
Sequence 9, Appl
Sequence 12, Appl
Sequence 3, Appli

24 2 US-09-962-360B-8
17 1 US-08-743-894B-27
17 1 US-08-743-894B-30
17 1 US-08-743-894B-32
17 1 US-08-743-894B-39
12 1 US-08-743-894B-41
13 2 US-09-976-535A-13
15 1 US-08-743-894B-38
15 1 US-08-743-894B-25
17 1 US-08-743-894B-24
17 1 US-08-743-894B-28
17 1 US-08-743-894B-29
17 1 US-08-743-894B-36
17 1 US-08-743-894B-42
17 1 US-08-743-894B-50
16 1 US-08-743-894B-9
16 1 US-08-743-894B-12
17 1 US-08-743-894B-3

ALIGNMENTS

RESULT 1

US-09-976-535A-1
; Sequence 1, Application US/09976535A
; Patent No. 6504006
; GENERAL INFORMATION:
; APPLICANT: Shine, Nancy R.
; APPLICANT: Crawford, Karen R.
; APPLICANT: Eaton, Linda J.
; TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteolytic Activity of Serotype A Neurotoxin from Clostridium botulinum
; FILE REFERENCE: P010018
; CURRENT APPLICATION NUMBER: US/09/976,535A
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: human
US-09-976-535A-1

Query Match 100.0%; Score 59; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANQRATKM 12

Db 2 RIDEANQRATKM 13

RESULT 2

US-08-743-894B-49
; Sequence 49, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin from Clostridium botulinum
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn: John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0

```
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA: US/08/743,894B
; APPLICATION NUMBER: 34,616
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
US-08-743-894B-49
;
Query Match 100.0%; Score 59; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.9e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIDEANQRATKM 12
Db 5 RIDEANQRATKM 16

RESULT 3
US-08-743-894B-1
; Sequence 1, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
```

```
; TOPOLOGY: Linear
;
US-08-743-894B-1
;
Query Match 100.0%; Score 59; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIDEANQRATKM 12
Db 5 RIDEANQRATKM 16

RESULT 4
US-08-743-894B-19
; Sequence 19, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 4
; OTHER INFORMATION: Xaa represents Abu, or 2-Aminobutyric Acid
;
US-08-743-894B-19
;
Query Match 100.0%; Score 59; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIDEANQRATKM 12
Db 5 RIDEANQRATKM 16

RESULT 5
US-08-743-894B-37
; Sequence 37, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
```

```
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
; US-08-743-894B-37
;
; Query Match 100.0%; Score 59; DB 1; Length 17;
; Best Local Similarity 100.0%; Pred. No. 0.00011;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 RIDEANORATKM 12
; Db 5 RIDEANQRATKM 16
;
; RESULT 6
; US-08-819-286-9
; Sequence 9, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-819-286-8
;
; Query Match 100.0%; Score 59; DB 2; Length 26;
; Best Local Similarity 100.0%; Pred. No. 0.00017;
;
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
; US-08-743-894B-37
;
; Query Match 100.0%; Score 59; DB 1; Length 17;
; Best Local Similarity 100.0%; Pred. No. 0.00011;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 RIDEANORATKM 12
; Db 5 RIDEANQRATKM 16
;
; RESULT 7
; US-08-819-286-8
; Sequence 8, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-819-286-8
;
; Query Match 100.0%; Score 59; DB 2; Length 26;
; Best Local Similarity 100.0%; Pred. No. 0.00017;
```

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
Db 11 RIDEANORATKM 22

RESULT 8

US-08-819-286-4
; Sequence 4, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-4

Query Match 100.0%; Score 59; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
Db 22 RIDEANORATKM 33

RESULT 9

US-08-760-001-10
; Sequence 10, Application US/08760001
; Patent No. 5962637
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,001
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-760-001-10

Query Match 100.0%; Score 59; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
Db 55 RIDEANORATKM 66

RESULT 10

US-09-015-960-10
; Sequence 10, Application US/09015960
; Patent No. 6043042
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,960
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/760,001
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

```
; NAME: Remond, Robert W.
; REGISTRATION NUMBER: 32,893
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-015-960-10

Query Match 100.0%; Score 59; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANQRATKM 12
Db 55 RIDEANQRATKM 66

RESULT 11
US-09-534-572-10
; Sequence 10, Application US/09534572
; Patent No. 6337386
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Basam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,572
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,960
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE: 30-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: peptide
; US-09-534-572-10

Query Match 100.0%; Score 59; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANQRATKM 12
Db 55 RIDEANQRATKM 66

RESULT 12
US-09-962-360B-11
; Sequence 11, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
; US-09-962-360B-11

Query Match 100.0%; Score 59; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANQRATKM 12
Db 100 RIDEANQRATKM 111

RESULT 13
US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Scheller, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
```

```
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-393-985-18

Query Match      100.0%; Score 59; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RIDEANORATKM 12
Db      191 RIDEANORATKM 202

RESULT 15
US-09-949-016-6311
; Sequence 6311, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6311
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6311

Query Match      100.0%; Score 59; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RIDEANORATKM 12
Db      191 RIDEANORATKM 202

Search completed: April 3, 2006, 15:33:15
Job time : 9.57798 secs
```

```
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-393-985-18

Query Match      100.0%; Score 59; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RIDEANORATKM 12
Db      191 RIDEANORATKM 202

RESULT 14
US-08-819-286-1
; Sequence 1, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-1

Query Match      100.0%; Score 59; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:27:42 ; Search time 61.8716 Seconds
(without alignments)
136.837 Million cell updates/sec

Title: US-09-942-098-2_COPY_191_202
Perfect score: 59
Sequence: 1 RIDEANQRATKM 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	59	100.0	124	2	O93578 BRARE	O93578 brachydanio
2	59	100.0	134	2	O48B5 TETNG	O48B5 tetraodon n
3	59	100.0	143	2	Q9GM34 MACFA	Q9GM34 macaca fasc
4	59	100.0	198	2	Q6PC84 BRARE	Q6PC84 brachydanio
5	59	100.0	203	1	SN25B CARAU	P36978 carassius a
6	59	100.0	203	2	O93579 BRARE	O93579 brachydanio
7	59	100.0	203	2	Q6PC54 BRARE	Q6PC54 brachydanio
8	59	100.0	204	1	SN25A CARAU	P36977 carassius a
9	59	100.0	204	2	Q705J6 LATJA	Q705J6 lateolabrax
10	59	100.0	204	2	Q5T266 BRARE	Q5T266 brachydanio
11	59	100.0	204	2	Q5T265 BRARE	Q5T265 brachydanio
12	59	100.0	206	1	SN255 CHICK	P60878 gallus gall
13	59	100.0	206	1	SNP25 HUMAN	P60880 homo sapien
14	59	100.0	206	1	SNP25 MACMU	P60877 macaca mula
15	59	100.0	206	1	SNP25 MOUSE	P60879 mus musculus
16	59	100.0	206	1	SNP25 PANTR	Q5R1X1 pan troglod
17	59	100.0	206	1	SNP25 RAT	P60881 rattus norv
18	59	100.0	206	2	Q53EM2 HUMAN	Q53EM2 homo sapien
19	59	100.0	206	2	Q5U0B5 HUMAN	Q5U0B5 homo sapien
20	59	100.0	206	2	Q5NVG5 PONGY	Q5NVG5 pongo pygma
21	59	100.0	206	2	Q5NVK3 PONGY	Q5NVK3 pongo pygma
22	59	100.0	206	2	Q5R690 PONGY	Q5R690 pongo pygma
23	59	100.0	206	2	Q5R6U7 PONGY	Q5R6U7 pongo pygma
24	59	100.0	206	2	Q4R4U6 MACFA	Q4R4U6 macaca fasc
25	59	100.0	236	2	Q4V509 CARAU	Q4V509 carassius a
26	55	93.2	204	2	Q6F3L7 BRARE	Q6F3L7 brachydanio
27	52	88.1	206	2	Q5R505 PONGY	Q5R505 pongo pygma
28	51	86.4	137	2	Q66ID7 BRARE	Q66ID7 brachydanio
29	51	86.4	186	2	Q4V9B7 BRARE	Q4V9B7 brachydanio
30	51	86.4	209	2	Q4V9B6 BRARE	Q4V9B6 brachydanio
31	51	86.4	214	2	Q7ZVE4 BRARE	Q7ZVE4 brachydanio

32	51	86.4	230	2	Q4REP6 TETNG	O4rep6 tetraodon n
33	50	84.7	206	2	Q640W4 XENLA	Q640w4 xenopus lae
34	50	84.7	206	2	Q8AXM1 XENLA	Q8axm1 xenopus lae
35	50	84.7	206	2	Q8AXM2 XENLA	Q8axm2 xenopus lae
36	50	84.7	210	1	SNP25 TORMA	P36976 torpedo mar
37	49	83.1	212	2	Q8T3S4 LOLPE	Q8t3s4 loligo peal
38	42	71.2	220	2	Q8G9G6 LYMST	Q8g9g6 lymnaea eta
39	41	69.5	55	2	Q8NCR8 HUMAN	Q8ncr8 homo sapien
40	41	69.5	83	2	Q85431 PSEPD	Q85431 pseudomonas
41	41	69.5	83	2	Q85439 PSEPL	Q85439 pseudomonas
42	41	69.5	83	2	Q85440 PSETO	Q85440 pseudomonas
43	41	69.5	191	2	Q8ZY72 PYRAE	Q8zy72 pyrobaculum
44	41	69.5	204	2	Q8JIS7 XENLA	Q8jis7 xenopus lae
45	40	67.8	577	2	Q5S6L2 VIBF1	Q5s6l2 vibrio fisc

ALIGNMENTS

RESULT 1
O93578 BRARE
ID O93578 BRARE PRELIMINARY; PRT; 124 AA.
AC O93578;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Synaptosome-associated protein 25.1 (Fragment).
GN Name=snap25a; Synonyms=Snap;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RX DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNR1>3.3.CO;2-Z;
RA Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
RA Larhammar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish:
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage.";
RL EMBL; AF091593; AAC64289.1; -; mRNA.
DR HSSP; Q8T3S4; 1L4A.
DR SMR; O93578; 49-122.
DR ENSEMBL; ENSDARG0000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR GO; GO:0019717; C:synaptosome; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002197; HTH_Ris.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR PRINTS; PR01590; HTHFIS.
DR SMART; SM00397; t_SNARE; 1.
DR PROSITE; PS50192; T_SNARE; 1.
DR NON TER
KW Synaptosome.
FT SEQUENCE 124 AA; 13616 MW; 50E27DBDB33D958C CRC64;
SQ SEQUENCE 124 AA; 13616 MW; 50E27DBDB33D958C CRC64;

Query Match 100.0%; Score 59; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 0.0086;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RIDEANQRATKM 12
| | | | | | | | | |
DB 109 RIDEANQRATKM 120
| | | | | | | | | |

RESULT 2

KW Synaptosome.
SQ SEQUENCE 198 AA; 22209 MW; 8FED509A00E1EC0 CRC64;
Query Match 100.0%; Score 59; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIDEANORATKM 12
DB 183 RIDEANORATKM 194
|||||

RESULT 5
SN25B CARAU STANDARD; PRT; 203 AA.
AC P36978;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptosomal-associated protein 25B (SNAP-25B).
GN Name=SNAP-B;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RX MEDLINE=94068448; PubMed=8248151;
RA Risinger C., Larhammar D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish."
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC -1- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
CC -1- SUBCELLULAR LOCATION: Complexed with macromolecular elements of the nerve terminal.
CC -1- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, and piriform cortex, anterior thalamic nuclei, pontine nuclei, and granule cells of the cerebellum.
CC -1- SIMILARITY: Belongs to the SNAP-25 family.
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC EMBL; L22976; AAA16538.1; -; mRNA.
CC PIR; I50481; I50481.
CC HSP; P13795; 1SPC.
CC SMR; P36978; 7-82, 128-201.
CC InterPro; IPR000928; SNAP-25.
CC Pfam; PF00835; SNAP-25; 1.
CC Pfam; PF05739; SNARE; 1.
CC SMART; SM00397; t-SNARE; 2.
CC PROSITE; PS50192; t-SNARE; 2.
CC Coiled coil; Glycoprotein; Multigene family; Repeat; Synaptosome.
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 137 199 t-SNARE coiled-coil homology 2.
FT COMPBIA 85 92 Cys-rich.
FT CARBOHYD 77 77 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 185 185 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 203 AA; 22664 MW; 8DFBBDDBED37D6D7 CRC64;
Query Match 100.0%; Score 59; DB 1; Length 203;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIDEANORATKM 12
DB 188 RIDEANORATKM 199
|||||

RESULT 6
O93579 BRARE PRELIMINARY; PRT; 203 AA.
AC O93579;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein 25.2.
GN Name=snap25b; Synonym=Snap;
OS Brachydanio rerio (Zebrafish)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99057281; PubMed=98431147;
RX DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNRI>3.3.CO;2-Z;
RA Risinger C., Salanek E., Soderberg C., Gates M., Postlethwait J.H., Larhammar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish: comparison of paralogous linkage groups suggests loss of one locus in the mammalian lineage";
RL J. Neurosci. Res. 54:563-573(1998).
DR EMBL; AF091594; AAC64290.1; -; mRNA.
DR HSP; P60881; 1JTH.
DR SMR; O93579; 7-82, 128-201.
DR ZFIN; ZDB-GENE-980526-392; snap25b.
DR GO; GO:001917; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; t-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; t-SNARE; 2.
KW Synaptosome.
SQ SEQUENCE 203 AA; 22647 MW; 93B7590DD0C93F38 CRC64;
Query Match 100.0%; Score 59; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIDEANORATKM 12
DB 188 RIDEANORATKM 199
|||||

RESULT 7
O6PC54 BRARE PRELIMINARY; PRT; 203 AA.
AC O6PC54;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Synaptosome-associated protein 25 b.
GN Name=snap25b;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=Wild-type; TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

```

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin I.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Wild-type; TISSUE=Eye;
RA Strauberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059469; AAH59469.1; -; mRNA.
DR ZFIN; ZDB-GENE-980526-392; snap25b.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
KW Synaptosome.
SQ SEQUENCE 203 AA; 22693 MW; 48D7590DD0C1179A CRC64;

Query Match 100.0%; Score 59; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANQORATKM 12
Db |||||

RESULT 8
SN25A_CARAU STANDARD; PRT; 204 AA.
AC P36977;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptosomal-associated protein 25A (SNAP-25A).
GN Name=SNAP-A;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Retina;
RX MEDLINE=94068448; PubMed=8248151;
RT Risinger C., Latham D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid
RT goldfish."
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC -1- FUNCTION: May play an important role in the synaptic function of
CC specific docking and membrane fusion.
CC -1- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
CC the nerve terminal.
CC -1- SIMILARITY: Belongs to the SNAP-25 family.
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

```

```

CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; L22973; AAA16537.1; -; mRNA.
DR PIR; I50480; I50480.
DR HSP; P13795; IN78.
DR SMR; P36977; 7-83, 129-202.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
KW Coiled coil; Multigene family; Repeat; Synaptosome.
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 138 200 t-SNARE coiled-coil homology 2.
FT COMPRTAS 85 92 Cys-rich.
SQ SEQUENCE 204 AA; 22843 MW; 458BBECFCFC09189 CRC64;

Query Match 100.0%; Score 59; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANQORATKM 12
Db |||||

RESULT 9
Q705J6_LATJA LATJA PRELIMINARY; PRT; 204 AA.
AC Q705J6;
DT 05-JUL-2004 (T:EMBLrel. 27, Created)
DT 05-JUL-2004 (T:EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T:EMBLrel. 27, Last annotation update)
DE Synaptosomal-associated protein 25.
GN Name=snap-25;
OS Lateolabrax japonicus (Japanese sea perch) (Japanese sea bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Lateolabrax.
OX NCBI_TaxID=8164;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RA Chen K., Huang X.H.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ619993; CAF04071.1; -; mRNA.
DR SMR; Q705J6; 7-83, 129-202.
DR GO; GO:0003700; F:translation factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 204 AA; 22842 MW; 8P77B18D519509B2 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANQORATKM 12
Db |||||

```

```
RESULT 10
Q5TZ66 BRARE PRELIMINARY; PRT; 204 AA.
ID Q5TZ66;
AC Q5TZ66;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Synaptosomal-associated protein (SNAP).
DE Synaptosomal-associated protein (SNAP).
GN Name=snap25a; Synonyms=OTTDARP0000005563; ORFNames=DKEYP-8F4.6-001;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lovell J.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Donaldson S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX465184; CAH69031.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69031.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69031.1; JOINED; Genomic DNA.
DR EMBL; BX465184; CA121359.1; JOINED; Genomic DNA.
DR SMR; Q5TZ66; 7-83, 129-202.
DR Ensembl; ENSDARG0000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR Pfam; PF00835; SNAP-25; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; t_SNARE; 2.
KW Synaptosome.
SQ SEQUENCE 204 AA; 22857 MW; B53CF5FD1C69EA5 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
Db 189 RIDEANORATKM 200

RESULT 11
Q5TZ65 BRARE PRELIMINARY; PRT; 204 AA.
ID Q5TZ65;
AC Q5TZ65;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Synaptosomal-associated protein (SNAP).
DE Synaptosomal-associated protein (SNAP).
GN Name=snap25a; Synonyms=OTTDARP0000005690; ORFNames=DKEYP-8F4.6-002;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lovell J.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Donaldson S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX465184; CAH69032.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69032.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69032.1; JOINED; Genomic DNA.
```

```
DR EMBL; BX465184; CA121360.1; JOINED; Genomic DNA.
DR SMR; Q5TZ65; 7-83, 129-202.
DR Ensembl; ENSDARG0000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; t_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR SMART; SM00397; t_SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; t_SNARE; 2.
KW Synaptosome.
SQ SEQUENCE 204 AA; 22878 MW; FBC79AB7015AC0ED CRC64;

Query Match 100.0%; Score 59; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
Db 189 RIDEANORATKM 200

RESULT 12
SNP25_CHICK STANDARD; PRT; 206 AA.
ID SNP25_CHICK STANDARD; PRT; 206 AA.
AC P60878; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
DE 25 kDa protein) (Super protein) (SUP).
GN Name=SNAP25; Synonyms=SNAP;
OS Gallus gallus (Chicken)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM SNAP25B).
RC STRAIN=White leghorn; TISSUE=Retina;
MEDLINE=91126080; PubMed=1992470;
RA Catsicas S.; Lathammar D.; Blomqvist A.G.; Sanna P.P.; Milner R.J.;
RA Wilson M.C.;
RA "Expression of a conserved cell-type-specific protein in nerve
RA terminals coincides with synaptogenesis."
RA Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS SNAP25A AND SNAP25B).
MEDLINE=93389738; PubMed=8377193;
RA Bark I.C.;
RA "Structure of the chicken gene for SNAP-25 reveals duplicated exon
RA encoding distinct isoforms of the protein."
RA J. Mol. Biol. 233:67-76(1993).
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion (By
CC similarity).
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1
CC and SNAP25BP. Binds STXB6. Found in a ternary complex with STX1A
CC and VAMP8 (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60878-1, P13795-1;
CC Sequence=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60878-2, P13795-2;
```

```
CC      Sequence=VSP_010018;
CC      -i- PFM: Palmitoylated (By similarity).
CC      -i- SIMILARITY: Belongs to the SNAP-25 family.
CC      -i- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; M57957; AAA49072.1; -; mRNA.
DR      EMBL; L09253; AAA49070.1; -; Genomic DNA.
DR      EMBL; L09254; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09257; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09259; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09251; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09258; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09250; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09253; AAA49071.1; -; Genomic DNA.
DR      EMBL; L09254; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09257; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09259; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09252; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09258; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09250; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09253; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09254; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09257; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09259; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09252; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09258; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09250; AAA49071.1; JOINED; Genomic DNA.
DR      PIR; A37861; A37861.
DR      SMR; P60878; 7-83, 131-204.
DR      InterPro; IPR000928; SNAP-25.
DR      InterPro; IPR000727; T-SNARE.
DR      Pfam; PF00835; SNAP-25_1.
DR      Pfam; PF05739; SNAP-25_1.
DR      SMART; SM00397; t-SNARE; 2.
DR      PROSITE; PS0192; T-SNARE; 2.
KW      Alternative splicing; Coiled coil; Lipoprotein; Palmitate;
KW      Phosphorylation; Repeat; Synaptosome.
FT      DOMAIN 19 81
FT      DOMAIN 140 202
FT      COMPBIAS 85 92
FT      SITE 180 181
FT      MOD RES 138 138
FT      MOD RES 187 187
FT      VARSPIC 58 89
FT      FTID=VSP_010018.
FT      FTID=VSP_010018.
SQ      SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
Query Match 100.0%; Score 59; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 RIDEANQRATKM 12
Db      191 RIDEANQRATKM 202
RESULT 13
SNP25 HUMAN STANDARD; PRT; 206 AA.
AC P60880; P13795; P36974; P70557; P70558; Q81XK3; Q96FW2; Q9BR45;
ID 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
DE 25 kDa protein) (Super protein) (SUP).
GN Name=SNAP25; Synonyms=SNAP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
```

```
RP NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A AND SNAP-25B).
RC TISSUE=Brain;
RX MEDLINE=94156217; PubMed=8112622; DOI=10.1016/0378-1119(94)90773-0;
RA Bark I.C., Wilson M.C.;
RT "Human cDNA clones encoding two different isoforms of the nerve
RL terminal protein SNAP-25.";
RN Gene 139:291-292(1994).
[2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A).
RC TISSUE=Brain;
RX MEDLINE=94333829; PubMed=8056350; DOI=10.1016/0378-1119(94)90027-2;
RA Zhao N., Hashida H., Takahashi N., Sakaki Y.;
RT "Cloning and sequence analysis of the human SNAP25 cDNA.";
RN Gene 145:313-314(1994).
[3]
RP NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.
RC TISSUE=Skeletal muscle;
RX MEDLINE=96332494; PubMed=8760387;
RA Jagadeish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H.,
RA Grusovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J.,
RA Ward C.W.;
RT "Insulin-responsive tissues contain the core complex protein SNAP-25
RT (synaptosomal-associated protein 25) A and B isoforms in addition to
RL syntaxin 4 and synaptobrevins 1 and 2.";
RN Biochem. J. 317:945-954(1996).
[4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A.G., Cowile G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaeslaih M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McMay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RN Nature 414:865-871(2001).
[5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25A).
RC TISSUE=Eye;
RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
```

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.",
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 11-81 AND 141-202 IN COMPLEX
RP WITH STX1A, CPLX1 AND VAMP2, AND NMR ANALYSIS.
RX MEDLINE=21822661; PubMed=11832227; DOI=10.1016/S0896-6273(02)00583-4;
RY Chen X., Tomchick D.R., Kovrigin E., Arac D., Machius M.,
RA Suedhof T.C., Rizo J.,
RT "Three-dimensional structure of the complexin/SNARE complex.",
RL Neuron 33:397-409(2002).
CC -!- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion.
CC -!- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
CC SNAP25BP and HGS. Binds STXB96. Found in a ternary complex with
CC STX1A and VAMP8 (By similarity).
CC -!- INTERACTION:
CC Q8TUN5:HIP14; NPExp=1; IntAct=EBI-524785, EBI-524753;
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms=2;
CC Comment=isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60880-1, P13795-1;
CC Sequence=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60880-2, P13795-2;
CC Sequence=VSP_006186;
CC -!- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, and
CC piriform cortex, anterior thalamic nuclei, pontine nuclei, and
CC granule cells of the cerebellum.
CC -!- PTM: Palmitoylated (By similarity).
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; L19760; AAC37545.1; -; mRNA.
CC EMBL; L19761; AAC37546.1; -; mRNA.
CC EMBL; D21267; BAA22370.1; -; mRNA.
CC EMBL; AL023913; CAC34534.1; -; Genomic DNA.
CC EMBL; AL023913; CAC34535.1; -; Genomic DNA.
CC EMBL; AL023913; CAD56158.1; -; Genomic DNA.
CC EMBL; AL023913; CAB42860.1; -; Genomic DNA.
CC EMBL; BC010647; AAH10647.1; -; mRNA.
CC EMBL; F15735; I53735.
CC PIR; I5735; I53735.
CC PDB; 1K1L; X-ray; C=11-80, D=141-203.
CC PDB; 1XTG; X-ray; B=146-204.
CC SMR; P60880; 7-83, 131-204.
CC IntAct; P60880; -.
CC Ensembl; ENSG00000132639; Homo sapiens.
CC HGNC; HGNC:11132; SNAP25.
CC H-InvDB; HIX0015639; -.
CC MIM; 600322; -.
CC GO; GO:0007269; P:neurotransmitter secretion; NAS.
CC GO; GO:0001504; P:neurotransmitter uptake; NAS.
CC GO; GO:0050796; P:regulation of insulin secretion; TAS.
CC GO; GO:0007268; P:synaptic transmission; NAS.
CC GO; GO:0016081; P:synaptic vesicle docking during exocytosis; NAS.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T_SNARE.

DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS0192; T_SNARE; 2.
KW 3D-structure; Alternative splicing; Coiled coil; Lipoprotein;
KW Palmitate; Phosphorylation; Repeat; Synaptosome.
FT DOMAIN 19 81
FT t-SNARE coiled-coil homology 1.
FT t-SNARE coiled-coil homology 2.
FT Cys-rich.
FT SITE 85 92
FT Cleavage (by BONT/E).
FT SITE 180 181
FT Phosphothreonine (By similarity).
FT MOD_RES 138 138
FT Phosphoserine (By similarity).
FT MOD_RES 187 187
FT ERIEKGMDQINKDKAEKKNLTDLGKFGCLV -> DRVEE
FT VARSPPLIC 58 89
FT GMNHINQDMKEAKKNLKDGLKCCGLFI (in isoform
FT SNAP-25a).
FT /FTId=VSP_006186.
FT HELIX 7 82
FT HELIX 142 201
FT TURN 202 202
FT t-SNARE coiled-coil homology 1.
SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
Query Match 100.0%; Score 59; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RIDEANQRAATKM 12
Db 191 RIDEANQRAATKM 202
RESULT 14
SNP25 MACMU STANDARD; PRT; 206 AA.
ID SNP25 MACMU STANDARD; PRT; 206 AA.
AC P60877; P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (synaptosomal-associated
DE 25 kDa protein).
GN Name=SNAP25;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hippocampus;
RA Jensen M.J., Smith L.A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion (By
CC similarity).
CC -!- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
CC SNAP25BP and HGS. Binds STXB96. Found in a ternary complex with
CC STX1A and VAMP8 (By similarity).
CC -!- PTM: Palmitoylated (By similarity).
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF240770; AAF64477.1; -; mRNA.
CC SMR; P60877; 7-83, 131-204.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T_SNARE.

CC -i- PTM: Palmitoylated (By similarity).
 CC -i- SIMILARITY: Belongs to the SNAP-25 family.
 CC -i- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; M22012; AAA61741.1; -; mRNA.
 CC EMBL; AF483516; AAL90790.1; -; mRNA.
 CC EMBL; AF483517; AAL90791.1; -; mRNA.
 CC EMBL; AK078038; BAC37105.1; -; mRNA.
 CC EMBL; BC018249; AAH18249.1; -; mRNA.
 CC FIR; A33623; A33623.
 CC PDB; 2BU0; Model; C=18-82, D=139-206.
 CC SMR; P60879; 7-83, 131-204.
 CC Ensembl; ENSMUSG0000027273; Mus musculus.
 CC MGI; MGI-98331; Snap25.
 CC GO; GO:0005886; C:plasma membrane; TAS.
 CC GO; GO:0000149; F:SNARE binding; IDA.
 CC GO; GO:0007269; P:neurotransmitter secretion; IMP.
 CC InterPro; IPR000928; SNAP-25.
 CC InterPro; IPR000727; T-SNARE.
 CC Pfam; PF00835; SNAP-25; 1.
 CC Pfam; PF05739; SNARE; 1.
 CC SMART; SM00397; t-SNARE; 2.
 CC PROSITE; PS0192; T-SNARE; 2.
 CC 3D-structure; Alternative splicing; Coiled coil; Lipoprotein;
 CC Palmitate; Phosphorylation; Repeat; Synaptosome.
 CC DOMAIN 19 81 t-SNARE coiled-coil homology 1.
 CC DOMAIN 140 202 t-SNARE coiled-coil homology 2.
 CC Cys-rich.
 CC SITE 85 92 Cleavage (by BONT/E) (By similarity).
 CC SITE 180 181 Phosphothreonine (by PKC and PKA).
 CC MOD RES 138 138 Phosphoserine (by PKC).
 CC MOD RES 187 187 Phosphoserine (by PKC).
 CC VARSPIC 58 89 ERIEGMDQINKMKAEKNTDLGKFCGLCV -> DRVVEE
 CC FT GNNHINQDMKEAKENLKDLGKCCGLFI (in isoform
 CC FT SNAP-25a).
 CC FT /FTid=VSP_010019.
 CC SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;

Query Match 100.0%; Score 59; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANQRATKM 12
 Db 191 RIDEANQRATKM 202

Search completed: April 3, 2006, 15:46:25
 Job time : 61.8716 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:30:10 ; Search time 6.49541 Seconds

(without alignments)
177.756 Million cell updates/sec

Title: US-09-942-098-2_COPY_191_202

Perfect score: 59

Sequence: 1 RIDEANQRATKM 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	203	2 I50481	synapse protein SN
2	59	100.0	204	2 I50480	synapse protein SN
3	59	100.0	206	2 A37861	synaptosomal-assoc
4	59	100.0	206	2 I53735	nerve terminal pro
5	59	100.0	206	2 I67823	nerve terminal pro
6	59	100.0	206	2 A36223	synaptosomal-assoc
7	50	84.7	210	2 I50552	synapse protein -
8	38	64.4	83	2 A33854	outer membrane lip
9	36	61.0	158	2 JCS297	vesicle-membrane f
10	36	61.0	210	2 JCS512	SNARE protein 23 -
11	36	61.0	211	2 JCS296	vesicle-membrane f
12	36	61.0	393	2 T32127	hypothetical prote
13	36	61.0	540	2 T34187	hypothetical prote
14	35	59.3	71	2 D84748	hypothetical prote
15	35	59.3	331	2 T05428	hypothetical prote
16	35	59.3	425	2 D84888	hypothetical prote
17	35	59.3	1223	2 T17345	hypothetical prote
18	35	59.3	1578	2 S76238	SyB2 transcriptio
19	34	57.6	151	2 G95369	hypothetical prote
20	34	57.6	176	2 D72668	hypothetical prote
21	34	57.6	219	2 AB1996	transcription regu
22	34	57.6	270	2 AE3518	hypothetical prote
23	34	57.6	414	2 T26205	hypothetical prote
24	34	57.6	462	2 A46170	tektin A1 - sea ur
25	34	57.6	482	2 A96790	protein T33B.18
26	34	57.6	494	2 S64386	pre-mRNA splicing
27	34	57.6	576	2 S49376	hypothetical prote
28	34	57.6	590	2 D83063	hypothetical prote
29	34	57.6	783	2 T47909	hypothetical prote

30	34	57.6	852	2 T08416	disease resistance
31	34	57.6	950	2 S64405	MIC1 protein - yea
32	34	57.6	1404	2 E36788	hypothetical prote
33	34	57.6	1566	2 A43607	cell surface antig
34	34	57.6	2427	2 T16613	hypothetical prote
35	33	55.9	69	1 B56085	copper homeostasis
36	33	55.9	99	2 H97828	hypothetical prote
37	33	55.9	133	2 B70338	general secretion
38	33	55.9	150	2 T19447	hypothetical prote
39	33	55.9	154	2 E64504	hypothetical prote
40	33	55.9	159	2 A24733	myosin heavy chain
41	33	55.9	181	2 S70030	myosin heavy chain
42	33	55.9	182	2 PNO157	myosin heavy chain
43	33	55.9	231	2 PNO158	myosin heavy chain
44	33	55.9	241	1 RRNZ	phosphoprotein P -
45	33	55.9	241	1 RRNZ	

ALIGNMENTS

RESULT 1

I50481
synapse protein SNAP-25 - goldfish
C:Species: Carassius auratus (goldfish)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50481
R:Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A:Reference number: A49632; MUID:94068448; PMID:8248151
A:Accession: I50481
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-203 <RIS>
A:Cross-references: UNIPROT:P36978; UNIPARC:UPI0000135B03; GB:L22976; NID:G349430; PIDN:?
C:Genetics:
A:Gene: SNAP-25

Query Match 100.0%; Score 59; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RIDEANQRATKM 12

Db 188 RIDEANQRATKM 199

RESULT 2

I50480
synapse protein SNAP-25 - goldfish
C:Species: Carassius auratus (goldfish)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50480
R:Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A:Reference number: A49632; MUID:94068448; PMID:8248151
A:Accession: I50480
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-204 <RIS>
A:Cross-references: UNIPROT:P36977; UNIPARC:UPI0000135B02; GB:L22973; NID:G349426; PIDN:?
C:Genetics:
A:Gene: SNAP-25

Query Match 100.0%; Score 59; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RIDEANQRATKM 12

Db 189 RIDEANQRATKM 200

```
RESULT 3
A37861
synaptosomal-associated 25K protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
C;Accession: A37861
R;Catsicas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coincides with the expression of synaptophysin in the developing chicken brain
A;Reference number: A37861; MUID:91126080; PMID:1992470
A;Accession: A37861
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <CAT>
A;Cross-references: UNIPROT:P60878; UNIPARC:UPI0000001103; GB:M57957; NID:g212673; PIDN:
I53735
Query Match 100.0%; Score 59; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIDEANQRATKM 12
Db 191 RIDEANQRATKM 202
RESULT 4
I53735
nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I53735
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A;Reference number: I53735; MUID:94156217; PMID:8112622
A;Accession: I53735
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: UNIPROT:P60880; UNIPARC:UPI0000002B3DD; GB:L19760; NID:g307425; PIDN:
A;Gene: GDB:SNAP
A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2
Query Match 100.0%; Score 59; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIDEANQRATKM 12
Db 191 RIDEANQRATKM 202
RESULT 5
I67823
nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I67823
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A;Reference number: I53735; MUID:94156217; PMID:8112622
A;Accession: I67823
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: UNIPROT:P60880; UNIPARC:UPI0000001103; GB:L19761; NID:g307427; PIDN:
A;Gene: GDB:SNAP
```

```
A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2
Query Match 100.0%; Score 59; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIDEANQRATKM 12
Db 191 RIDEANQRATKM 202
RESULT 6
A33623
synaptosomal-associated 25K protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 09-Jul-2004
C;Accession: A33623
R;Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.; v
J. Cell Biol. 109, 3039-3052, 1989
A;Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differer
A;Reference number: A33623; MUID:90078337; PMID:2592413
A;Accession: A33623
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <OYL>
A;Cross-references: UNIPROT:P60879; UNIPARC:UPI0000001103; GB:M22012; GB:X51673; NID:g201
I50552
Query Match 100.0%; Score 59; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIDEANQRATKM 12
Db 191 RIDEANQRATKM 202
RESULT 7
I50552
synapse protein - marbled electric ray
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50552
R;Risager, C.; Blomqvist, A.G.; Lundell, I.; Lambertsson, A.; Nassel, D.; Pieribone, V.;
J. Biol. Chem. 268, 24408-24414, 1993
A;Title: Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25) shc
A;Reference number: A49513; MUID:94043281; PMID:8226991
A;Accession: I50552
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-210 <RIS>
A;Cross-references: UNIPROT:P36976; UNIPARC:UPI0000135AFE; GB:L22020; NID:g431296; PIDN:
I50552
Query Match 84.7%; Score 50; DB 2; Length 210;
Best Local Similarity 83.3%; Pred. No. 0.049;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RIDEANQRATKM 12
Db 198 RIDEANQRATKM 209
RESULT 8
A33854
outer membrane lipoprotein I precursor - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 09-Jul-2004
C;Accession: A33854; S04834; A44834; A83288
R;Duchene, M.; Barron, C.; Schweizer, A.; von Specht, B.U.; Domdey, H.
J. Bacteriol. 171, 4130-4137, 1989
A;Title: Pseudomonas aeruginosa outer membrane lipoprotein I gene: molecular cloning, seq
A;Reference number: A33854; MUID:89327122; PMID:2502533
A;Accession: A33854
```

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <DUC>
A;Cross-references: UNIPROT:P11221; UNIPARC:UPI0000002C273; GB:M25761; NID:g151334; PIDN:
R;Cornelis, P.; Bouia, A.; Belarbi, A.; Guyonvarch, A.; Kammerer, B.; Hannaert, V.; Hube
Mol. Microbiol. 3, 421-428, 1989
A;Title: Cloning and analysis of the gene for the major outer membrane lipoprotein from
A;Reference number: S04834; MUID:99313294; PMID:2473376
A;Accession: S04834
A;Molecule type: DNA
A;Residues: 1-83 <COR>
A;Cross-references: UNIPARC:UPI0000002C273; EMBL:X13748; NID:g45344; PIDN:CAA32013.1; PID
A;Note: the authors translated the codon GAA for residue 78 as Gly
R;Saint-Onge, A.; Roneyer, F.; Lebel, P.; Masson, L.; Brousseau, R.
J. Gen. Microbiol. 138, 733-741, 1992
A;Title: Specificity of the Pseudomonas aeruginosa PAO1 lipoprotein I gene as a DNA prob
A;Reference number: A44834; MUID:92268853; PMID:11588307
A;Accession: A44834
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <SAL>
A;Cross-references: UNIPARC:UPI0000002C273; GB:X58714; GB:S36066; NID:g433509; PIDN:CAA41
A;Experimental source: PAO1
A;Note: sequence extracted from NCBI backbone (NCBIN:103666, NCBI:P103667)
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A82950
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <STO>
A;Cross-references: UNIPARC:UPI0000002C273; GB:AE004712; GB:AE004091; NID:g9948940; PIDN:
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: oprI; PA2853
C;Keywords: lipid binding; lipoprotein; membrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-83/Product: lipoprotein I #status predicted <MAT>
Query Match 64.4%; Score 38; DB 2; Length 83;
Best Local Similarity 70.0%; Pred. No. 3.6; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 DEANORATKM 12
||| ||| :
Db 67 DEANERLRM 76
RESULT 9
JC5297
vesicle-membrane fusion protein SNAP-23B - human
C;Species: Homo sapiens (man)
C;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: JC5297
R;Mollinedo, F.; Lazo, P.A.
Biochem. Biophys. Res. Commun. 231, 808-812, 1997
A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23
A;Reference number: JC5296; MUID:97224437; PMID:9070898
A;Accession: JC5297
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-158 <MOL>
A;Cross-references: UNIPROT:O00161; UNIPARC:UPI000002B3DC; GB:Y09568; NID:g1924943; PIDN
A;Experimental source: neutrophils
C;Comment: This protein is involved in regulating exocytosis in human neutrophils, a cen
Query Match 61.0%; Score 36; DB 2; Length 158;
Best Local Similarity 66.7%; Pred. No. 17; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 RIDEANORATKM 12
||| ||| :
Db 144 RIDIANARAKKL 155
RESULT 10
JC5512
SNARE protein 23 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5512
R;Araki, S.; Tamori, Y.; Kawanishi, M.; Shinoda, H.; Masugi, J.; Mori, H.; Niki, T.; Oka;
Biochem. Biophys. Res. Commun. 234, 257-262, 1997
A;Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c.
A;Reference number: JC5512; MUID:97312558; PMID:9168999
A;Accession: JC5512
A;Molecule type: mRNA
A;Residues: 1-210 <ARA>
A;Cross-references: UNIPROT:O09044; UNIPARC:UPI000002B5C; DDBJ:AB000822; NID:g2189950; I
C;Comment: This protein is involved in the insulin-induced translocation of vesicles cont
Query Match 61.0%; Score 36; DB 2; Length 210;
Best Local Similarity 66.7%; Pred. No. 23; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 RIDEANORATKM 12
||| ||| :
Db 196 RIDIANTRAKKL 207
RESULT 11
JC5296
vesicle-membrane fusion protein SNAP-23A - human
C;Species: Homo sapiens (man)
C;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: JC5296
R;Mollinedo, F.; Lazo, P.A.
Biochem. Biophys. Res. Commun. 231, 808-812, 1997
A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23
A;Reference number: JC5296; MUID:97224437; PMID:9070898
A;Accession: JC5296
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-211 <MOL>
A;Cross-references: UNIPROT:O00161; UNIPARC:UPI0000000A2C; GB:Y09567; NID:g1924941; PIDN:
C;Comment: This protein is involved in regulating exocytosis in human neutrophils, a cent
Query Match 61.0%; Score 36; DB 2; Length 211;
Best Local Similarity 66.7%; Pred. No. 23; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 RIDEANORATKM 12
||| ||| :
Db 197 RIDIANARAKKL 208
RESULT 12
JC52127
hypothetical protein R07C3.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32127
R;Lamar, B.; Kramer, J.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid R07C3.
A;Reference number: Z31125
A;Accession: T32127
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393 <LAM>
A;Cross-references: UNIPROT:O16766; UNIPARC:UPI00001642E9; EMBL:AF016686; PIDN:AAB66239.1
A;Experimental source: strain Bristol N2; clone R07C3
C;Genetics:

A;Gene: CESP:R07C3.10
A;Map position: 2
A;Introns: 20/1; 350/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C32B5.10

Query Match 61.0%; Score 36; DB 2; Length 393;
Best Local Similarity 58.3%; Pred. No. 44;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RIDEANQQRATKM 12
|||::|||
Db 101 RIKEENEKITKM 112

RESULT 13

T34187

hypothetical protein C49H3.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 12-Jul-2004

C;Accession: T34187

R;Wu, X.

submitted to the EMBL Data Library, December 1995

A;Description: The sequence of C. elegans cosmid C49H3.

A;Reference number: Z21485

A;Accession: T34187

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-540 <WUX>

A;Cross-references: UNIPROT:Q9GYQ4; UNIPARC:UPI000017CE0F; EMBL:U42436; PIDN:AAA83492.1;

C;Genetics:

A;Gene: CESP:C49H3.1

A;Introns: 247/2; 319/2; 393/3

Query Match 61.0%; Score 36; DB 2; Length 540;
Best Local Similarity 54.5%; Pred. No. 61;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IDEANQQRATKM 12
::|||:::
Db 277 LEEANQRADRL 287

RESULT 14

D84748

hypothetical protein At2g33690 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: D84748

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: D84748

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-71 <STO>

A;Cross-references: UNIPROT:O23658; UNIPARC:UPI00000A2B44; GB:AE002093; NID:G2253578; PT

C;Genetics:

A;Gene: At2g33690

A;Map position: 2

Query Match 59.3%; Score 35; DB 2; Length 71;
Best Local Similarity 70.0%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IDEANQQRATK 11
|||::|||
Db 62 IDSANQKAKK 71

RESULT 15

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:27:08 ; Search time 61.5413 Seconds
(without alignments)
85.675 Million cell updates/sec

Title: US-09-942-098-2_COPY_191_202

Perfect score: 59

Sequence: 1 RIDEANQRATKM 12

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	13	AAE36672	AAE36672 Human SNA
2	59	100.0	13	ABW01728	ABW01728 Human SNA
3	59	100.0	13	ADM97043	ADM97043 Botulinum
4	59	100.0	13	AEA14917	AEA14917 Human SNA
5	59	100.0	16	AAV44069	AAV44069 Human SNA
6	59	100.0	16	AAE36736	AAE36736 Fret subs
7	59	100.0	16	AAE36739	AAE36739 Fret subs
8	59	100.0	16	AAE36674	AAE36674 Human SNA
9	59	100.0	16	ABW01795	ABW01795 FRET subs
10	59	100.0	16	ABW01730	ABW01730 Human SNA
11	59	100.0	16	ABW01792	ABW01792 FRET subs
12	59	100.0	16	ADM97045	ADM97045 Botulinum
13	59	100.0	16	ADM97061	ADM97061 Botulinum
14	59	100.0	16	AEA14919	AEA14919 Human SNA
15	59	100.0	17	AAV44057	AAV44057 Human SNA
16	59	100.0	17	AAV44039	AAV44039 Human SNA
17	59	100.0	17	AAV44021	AAV44021 Amino aci
18	59	100.0	17	ABG69065	ABG69065 Human pol
19	59	100.0	17	AAE36675	AAE36675 Human SNA
20	59	100.0	17	AAE36676	AAE36676 Human SNA
21	59	100.0	17	ABW01732	ABW01732 Human SNA
22	59	100.0	17	ABW01731	ABW01731 Human SNA
23	59	100.0	17	ADM97046	ADM97046 Botulinum
24	59	100.0	17	ADM97062	ADM97062 Botulinum

25	59	100.0	17	ADM97047	Adm97047 Botulinum
26	59	100.0	17	AEA14921	AEA14921 Human SNA
27	59	100.0	17	AEA14920	AEA14920 Human SNA
28	59	100.0	18	AAE36677	AAE36677 Human SNA
29	59	100.0	18	ABW01733	ABW01733 Human SNA
30	59	100.0	18	ADM97048	Adm97048 Botulinum
31	59	100.0	18	AEA14922	AEA14922 Human SNA
32	59	100.0	19	AAE15586	AAE15586 Human SNA
33	59	100.0	19	AAE36730	AAE36730 Fret subs
34	59	100.0	19	AAE36740	AAE36740 Fret subs
35	59	100.0	19	AAE36737	AAE36737 Fret subs
36	59	100.0	19	ABW01793	ABW01793 FRET subs
37	59	100.0	19	ABW01796	ABW01796 FRET subs
38	59	100.0	19	ABW01786	ABW01786 FRET subs
39	59	100.0	19	ADP13171	ADP13171 SNAP 25 p
40	59	100.0	20	AAW30100	AAW30100 Neurotran
41	59	100.0	20	ABW01798	ABW01798 FRET subs
42	59	100.0	21	AAE36734	AAE36734 Fret subs
43	59	100.0	21	ABW01790	ABW01790 FRET subs
44	59	100.0	22	AAE36738	AAE36738 Fret subs
45	59	100.0	22	ABW01794	ABW01794 FRET subs

ALIGNMENTS

RESULT 1

AAE36672
ID AAE36672 standard; peptide; 13 AA.

XX AC AAE36672;

XX 07-AUG-2003 (first entry)

XX Human SNAP-25 peptide #3.

XX Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
KW cosmetic.

XX Homo sapiens.

XX WO2003020948-A2.

XX 13-MAR-2003.

XX 22-AUG-2002; 2002WO-US027145.

XX 28-AUG-2001; 2001US-00942024.

XX (ALLR) ALLERGAN INC.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-290198/28.

PT Botulinum serotype A/E substrate useful for assaying protease activity of
PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
PT toxin recognition sequence that includes a cleavage site.

XX Disclosure; Page 40; 168pp; English.

XX The present invention relates to novel clostridium toxin substrates. The
CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
CC which comprise a donor fluorophore, an acceptor having an absorbance
CC spectrum overlapping the emission spectrum of the donor fluorophore, and a
CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
CC the cleavage site intervenes between the donor fluorophore and acceptor
CC and under the appropriate conditions, the resonance energy transfer is
CC exhibited between the donor and acceptor. Natural targets of clostridium
CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
CC of the invention are useful in assaying for the protease activity of any
CC clostridial toxin including botulinum toxins of all serotypes and tetanus

CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is human
 CC SNAP-25 peptide used in the invention

XX Sequence 13 AA;

Query Match 100.0%; Score 59; DB 6; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00022;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
 Db 2 RIDEANORATKM 13

RESULT 2
 ABW01728
 ID ABW01728 standard; peptide; 13 AA.

XX AC ABW01728;

XX 12-FEB-2004 (first entry)

XX Human SNAP-25 BoNT/A recognition peptide #1.

XX Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
 KW human.

XX Homo sapiens.

XX US2003143651-A1.

XX 31-JUL-2003.

XX 28-AUG-2001; 2001US-00942098.

XX 28-AUG-2001; 2001US-00942098.

XX (STEW/) STEWARD L E.

XX (FERN/) FERNANDEZ-SALAS E.

XX (AOKI/) AOKI K R.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-829791/77.

XX Determining clostridial toxin protease activity, by treating sample with
 PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
 PT sequence, under conditions which exhibit resonance energy transfer.

XX Disclosure; Page 10; Opp; English.

XX The present invention provides clostridial toxin substrates useful in
 CC assaying for the protease activity of any clostridial toxin including
 CC toxins of all serotypes as well as tetanus toxins. The present sequence
 CC is human SNAP-25 BoNT/A (botulinum neurotoxin serotype A) recognition
 CC peptide

XX Sequence 13 AA;

Query Match 100.0%; Score 59; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00022;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
 Db 2 RIDEANORATKM 13

RESULT 3
 ADM97043
 ID ADM97043 standard; peptide; 13 AA.

XX AC ADM97043;

XX 01-JUL-2004 (first entry)

XX Botulinum toxin substrate recognition sequence #28.

XX clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.

XX Synthetic.

XX WO2004029576-A2.

XX 08-APR-2004.

XX 04-SEP-2003; 2003WO-US028092.

XX 27-SEP-2002; 2002US-00261161.

XX (ALLR) ALLERGAN INC.

XX Fernandez-Salas E, Steward LE, Aoki KR;

XX WPI; 2004-340456/31.

XX Determining clostridial toxin activity, comprises contacting cell with
 PT sample comprising substrate with donor fluorophore, acceptor and
 PT recognition sequence, exciting fluorophore, and determining resonance
 PT energy transfer of contacted cell.

XX Disclosure; SEQ ID NO 49; 188pp; English.

XX The invention relates to a method of determining (M1) clostridial toxin
 CC activity, comprising contacting cell with sample comprising clostridial
 CC toxin substrate with donor fluorophore (F), acceptor (A) with an
 CC absorbance spectrum overlapping emission spectrum of fluorophore
 CC clostridial toxin recognition sequence with cleavage site intervening
 CC between (F) and (A), where under appropriate conditions resonance
 CC transfer is exhibited between fluorophore and acceptor, exciting the
 CC donor fluorophore, and determining resonance energy transfer of the
 CC contacted cell relative to a control cell, where a difference in
 CC resonance energy transfer of the contacted cell as compared to the
 CC control cell is indicative of clostridial toxin activity. (M1) is useful
 CC for determining clostridial toxin activity, where the sample is a crude
 CC cell lysate, isolated clostridial toxin, formulated clostridial toxin
 CC product, BOTOX or food. (M1) is an automated high-throughput assay. (M1)
 CC reduces the need for animal toxicity studies and serves to analyze
 CC multiple toxin functions such as binding a cellular uptake of the toxin,
 CC translocation into the cell cytosol and protease activity. In the method
 CC M1, the clostridial toxin substrate is a botulinum toxin substrate
 CC selected from a BoNT/A, BoNT/B, BoNT/C1, BoNT/D, BoNT/E, BoNT/F, BoNT/G
 CC or TeNT substrate comprising a BoNT/A, BoNT/B, BoNT/C1, BoNT/D, BoNT/E,
 CC BoNT/F, BoNT/G or TeNT recognition sequence. This sequence corresponds to
 CC a recognition sequence for a botulinum toxin used as the clostridial
 CC toxin substrate.

XX Sequence 13 AA;

Query Match 100.0%; Score 59; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00022;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANORATKM 12
 Db 2 RIDEANORATKM 13

RESULT 4

AE14917
ID AEA14917 standard; peptide; 13 AA.
XX
AC AEA14917;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human SNAP-25 substrate BoNT/A recognition sequence, SEQ ID NO: 27.
XX
KW Neurotoxin; fluorescence; SNAP-25; botulinum toxin.
XX
OS Homo sapiens.
XX
PN US2005100973-A1.
XX
PD 12-MAY-2005.
XX
PF 13-AUG-2004; 2004US-00917844.
XX
PR 28-AUG-2001; 2001US-00942098.
XX
PA (ALLR) ALLERGAN SALES INC.
XX
PI Steward LE, Gilmore MA, Aoki KR;
XX
DR WPI; 2005-365632/37.
XX
PT Determining clostridial toxin protease activity, by treating sample with
PT tagged toxin substrate comprising fluorescent protein, first and second
PT partner of affinity couple and assaying fluorescent cleavage product in
PT treated sample.
XX
PS Disclosure; SEQ ID NO 27; 97pp; English.
XX
CC The present invention relates to a method for determining protease
CC activity of clostridial neurotoxins such as botulinum neurotoxin (BoNT)
CC and tetanus neurotoxin (TeNT). The method involves treating with a
CC sample, in solution phase under conditions suitable for clostridial toxin
CC protease activity, a tagged toxin substrate (e.g. SNAP-25, VAMP,
CC syntaxin) comprising fluorescent protein, first partner of affinity
CC couple and clostridial toxin recognition sequence comprising cleavage
CC site; contacting treated sample with second partner of affinity couple;
CC and assaying presence of fluorescent cleavage product in the treated
CC sample. The present sequence is the human SNAP-25 substrate BoNT/A
CC (botulinum neurotoxin serotype A) recognition sequence.
XX
SQ Sequence 13 AA;
Query Match 100.0%; Score 59; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIDEANORATKM 12
DB 2 RIDEANORATKM 13
RESULT 5
AA44069
ID AAY44069 standard; peptide; 16 AA.
XX
AC AAY44069;
XX
DT 18-JAN-2000 (first entry)
XX
DE Human SNAP25 (amino acids 187-203) analogue [1-16].
XX
KW Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;
KW fluorescamine; detection; human; synaptosomal protein; SNAP25;
KW hydrolysis; amino group.
XX
OS Homo sapiens.
XX

US5965699-A.
12-OCT-1999.
06-NOV-1996; 96US-00743894.
06-NOV-1996; 96US-00743894.
(USSA) US SEC OF ARMY.
Bostian KA, Schmidt JJ;
WPI; 1999-579939/49.
Quantitation of type A botulinum toxin.
Disclosure; Col 13-14; 28pp; English.
XX
CC The invention relates to an enzymatic assay for the quantitation of type
CC A botulinum toxin, by determining the proteolytic activity of botulinum
CC neurotoxin type A using fluorescamine detection. Botulinum toxin A has
CC been shown to cleave the synaptosomal neurotransmitter peptide SNAP25
CC between residues 197-198. The method comprises adding an analogue (e.g.
CC AAY4022-Y44076) of the SNAP25 peptide (AAY44021, amino acids 187-203 of
CC human SNAP25) to a sample containing the botulinum toxin A so that
CC hydrolysis of the peptide is initiated, then stopping hydrolysis of the
CC peptide at different time points; and measuring the amount of hydrolysis
CC at each time point by combining with a label capable of detecting free
CC amino groups resulting from the hydrolysis. The amount of botulinum toxin
CC A present in the sample is determined by comparing measurements with the
CC amount of label produced from a known concentration of toxin measured of
CC under similar conditions. The method is useful for the quantitation of
CC type A botulinum toxin
XX
SQ Sequence 16 AA;
Query Match 100.0%; Score 59; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIDEANORATKM 12
DB 5 RIDEANORATKM 16
RESULT 6
AAE36736
ID AAE36736 standard; peptide; 16 AA.
XX
AC AAE36736;
XX
DT 07-AUG-2003 (first entry)
XX
DE Fret substrate peptide #7 used in the invention.
XX
KW Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
KW cosmetic.
XX
OS Unidentified.
XX
FH Key 1 Location/Qualifiers
FT Modified-site 1 /note= "Fluorescein-modified Lysine; This residue is
FT given as Xaa in the sequence shown as SEQ ID NO: 91 in
FT the sequence listing of the specification"
FT Modified-site 16
FT /note= "Tetramethylrhodamine-modified Lysine; C-terminal
FT amide; This residue is given as Xaa in the sequence shown
FT as SEQ ID NO: 91 in the sequence listing of the
FT specification"
XX
PN WO2003020948-A2.

XX 13-MAR-2003.
 PD 22-AUG-2002; 2002WO-US027145.
 XX 28-AUG-2001; 2001US-00942024.
 XX (ALLR) ALLERGAN INC.
 PA Steward LE, Fernandez-Salas E, Aoki KR;
 PI WPI; 2003-290198/28.
 DR Botulinum serotype A/E substrate useful for assaying protease activity of
 PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 PT toxin recognition sequence that includes a cleavage site.
 XX Example 1; Page 115; 168pp; English.
 PS The present invention relates to novel clostridium toxin substrates. The
 XX invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is fret
 CC substrate peptide used in the exemplification of the invention
 XX Sequence 16 AA;
 SQ Query Match 100.0%; Score 59; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00027;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIDEANQRATKM 12
 Db |||||
 3 RIDEANQRATKM 14
 RESULT 7
 AAE36739
 ID AAE36739 standard; peptide; 16 AA.
 AC AAE36739;
 XX 07-AUG-2003 (first entry)
 DT Fret substrate peptide #10 used in the invention.
 DE Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW cosmetic.
 XX Unidentified.
 OS Key Location/Qualifiers
 XX Modified-site 1
 FT /note= "DABCYL-modified Lysine; This residue is given as
 FT xaa in the sequence shown as SEQ ID NO: 94 in the
 FT sequence listing of the specification"
 FT Modified-site 16

FT /note= "EDANS-modified Glutamate; C-terminal amide; This
 FT residue is given as Xaa in the sequence shown as SEQ ID
 FT NO: 94 in the sequence listing of the specification"
 XX WO2003020948-A2.
 XX 13-MAR-2003.
 XX 22-AUG-2002; 2002WO-US027145.
 XX 28-AUG-2001; 2001US-00942024.
 XX (ALLR) ALLERGAN INC.
 PA Steward LE, Fernandez-Salas E, Aoki KR;
 PI WPI; 2003-290198/28.
 DR Botulinum serotype A/E substrate useful for assaying protease activity of
 PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 PT toxin recognition sequence that includes a cleavage site.
 XX Example 1; Page 115; 168pp; English.
 PS The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is fret
 CC substrate peptide used in the exemplification of the invention
 XX Sequence 16 AA;
 SQ Query Match 100.0%; Score 59; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00027;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIDEANQRATKM 12
 Db |||||
 3 RIDEANQRATKM 14
 RESULT 8
 AAE36674
 ID AAE36674 standard; peptide; 16 AA.
 AC AAE36674;
 XX 07-AUG-2003 (first entry)
 DT Human SNAP-25 peptide #5.
 DE Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW cosmetic.
 XX Homo sapiens.
 OS WO2003020948-A2.
 PN

XX 13-MAR-2003.
 XX PD
 XX PF
 XX PF 22-AUG-2002; 2002WO-US027145.
 XX PR 28-AUG-2001; 2001US-00942024.
 XX PA (ALLR) ALLERGAN INC.
 XX PI Steward LE, Fernandez-Salas E, Aoki KR;
 XX WIPI; 2003-290198/28.
 XX DR
 XX PT Botulinum serotype A/E substrate useful for assaying protease activity of
 XX PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 XX PT toxin recognition sequence that includes a cleavage site.
 XX PS Disclosure; Page 40; 168pp; English.
 XX CC The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is human
 CC SNAP-25 peptide used in the invention
 XX SQ Sequence 16 AA;
 Query Match 100.0%; Score 59; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00027;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIDEANQRATKM 12
 |||||
 5 RIDEANQRATKM 16
 Db
 RESULT 9
 ABW01795
 ID ABW01795 standard; peptide; 16 AA.
 XX AC ABW01795;
 XX DT 12-FEB-2004 (first entry)
 XX DE FRET substrate #8 to analyse proteolytic activity of botulinum toxin.
 XX KW Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
 XX KW FRET; fluorescence resonance energy transfer.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT Modified-site 16 /note= "DABCYL labelled lysine"
 FT Modified-site 16 /note= "EDANS labelled glutamate; C-terminal amide"
 XX US2003143651-A1.
 FN

XX 31-JUL-2003.
 XX PD
 XX PF 28-AUG-2001; 2001US-00942098.
 XX PR 28-AUG-2001; 2001US-00942098.
 XX PA (STEW/) STEWARD L E.
 XX PA (FERN/) FERNANDEZ-SALAS E.
 XX PA (AOKI/) AOKI K R.
 XX PI Steward LE, Fernandez-Salas E, Aoki KR;
 XX WIPI; 2003-829791/77.
 XX DR
 XX PT Determining clostridial toxin protease activity, by treating sample with
 XX PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
 XX PT sequence, under conditions which exhibit resonance energy transfer.
 XX PS Example 1; Page 29; Opp; English.
 XX CC The present invention provides clostridial toxin substrates useful in
 CC assaying for the protease activity of any clostridial toxin including
 CC toxins of all serotypes as well as tetanus toxins. The present sequence
 CC is FRET (fluorescence resonance energy transfer) substrate to analyse
 CC proteolytic activity of botulinum toxin. This substrate is used in the
 CC exemplification of the invention
 XX SQ Sequence 16 AA;
 Query Match 100.0%; Score 59; DB 7; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00027;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIDEANQRATKM 12
 |||||
 3 RIDEANQRATKM 14
 Db
 RESULT 10
 ABW01730
 ID ABW01730 standard; peptide; 16 AA.
 XX AC ABW01730;
 XX DT 12-FEB-2004 (first entry)
 XX DE Human SNAP-25 BoNT/A recognition peptide #3.
 XX KW Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
 XX KW human.
 XX OS Homo sapiens.
 XX XX US2003143651-A1.
 XX PD 31-JUL-2003.
 XX PF 28-AUG-2001; 2001US-00942098.
 XX PR 28-AUG-2001; 2001US-00942098.
 XX PA (STEW/) STEWARD L E.
 XX PA (FERN/) FERNANDEZ-SALAS E.
 XX PA (AOKI/) AOKI K R.
 XX PI Steward LE, Fernandez-Salas E, Aoki KR;
 XX WIPI; 2003-829791/77.
 XX DR
 XX PT Determining clostridial toxin protease activity, by treating sample with
 XX PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
 XX PT sequence, under conditions which exhibit resonance energy transfer.
 XX FN

XX Disclosure; Page 10; Opp; English.
PS
XX
CC The present invention provides clostridial toxin substrates useful in
CC assaying for the protease activity of any clostridial toxin including
CC toxins of all serotypes as well as tetanus toxins. The present sequence
CC is human SNAP-25 Bont/A (botulinum neurotoxin serotype A) recognition
CC peptide
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 59; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIDEANORATKM 12
Db 5 RIDEANORATKM 16
|||||

RESULT 11
ABW01792
ID ABW01792 standard; peptide; 16 AA.
XX
AC ABW01792;
XX
DT 12-FEB-2004 (first entry)
XX
DE FRET substrate #5 to analyse proteolytic activity of botulinum toxin.
XX
KW Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
KW FRET; fluorescence resonance energy transfer.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Fluoresceinated lysine"
FT Modified-site 16 /note= "Tetramethylrhodamine labelled lysine; C-terminal
FT amide"
XX
PN US2003143651-A1.
XX
PD 31-JUL-2003.
XX
PF 28-AUG-2001; 2001US-00942098.
XX
PR 28-AUG-2001; 2001US-00942098.
XX
PA (STEW/) STEWARD L E.
PA (FERN/) FERNANDEZ-SALAS E.
PA (AOKI/) AOKI K R.
XX
PI Steward LE, Fernandez-Salas E, Aoki KR;
XX
DR WPI; 2003-829791/77.
XX
XX Determining clostridial toxin protease activity, by treating sample with
PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
PT sequence, under conditions which exhibit resonance energy transfer.
XX
PS Example 1; Page 29; Opp; English.
XX
CC The present invention provides clostridial toxin substrates useful in
CC assaying for the protease activity of any clostridial toxin including
CC toxins of all serotypes as well as tetanus toxins. The present sequence
CC is FRET (fluorescence resonance energy transfer) substrate to analyse
CC proteolytic activity of botulinum toxin. This substrate is used in the
CC exemplification of the invention
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 59; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIDEANORATKM 12
Db 3 RIDEANORATKM 14
|||||

RESULT 12
ADM97045
ID ADM97045 standard; peptide; 16 AA.
XX
AC ADM97045;
XX
DT 01-JUL-2004 (first entry)
XX
DE Botulinum toxin substrate recognition sequence #30.
XX
KW clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.
XX
OS Homo sapiens.
XX
PN WO2004029576-A2.
XX
PD 08-APR-2004.
XX
PF 04-SEP-2003; 2003WO-US028092.
XX
PR 27-SEP-2002; 2002US-00261161.
XX
PA (ALLR) ALLERGAN INC.
XX
PI Fernandez-Salas E, Steward LE, Aoki KR;
XX
DR WPI; 2004-340456/31.
XX
XX Determining clostridial toxin activity, comprises contacting cell with
PT sample comprising substrate with donor fluorophore, acceptor and
PT recognition sequence, exciting fluorophore, and determining resonance
PT energy transfer of contacted cell.
XX
PS Disclosure; SEQ ID NO 51; 188pp; English.
XX
CC The invention relates to a method of determining (M1) clostridial toxin
CC activity, comprising contacting cell with sample comprising clostridial
CC toxin substrate with donor fluorophore (F), acceptor (A) with an
CC absorbance spectrum overlapping emission spectrum of fluorophore
CC clostridial toxin recognition sequence with cleavage site intervening
CC between (F) and (A), where under appropriate conditions resonance
CC transfer is exhibited between fluorophore and acceptor, exciting the
CC donor fluorophore, and determining resonance energy transfer of the
CC contacted cell relative to a control cell, where a difference in
CC resonance energy transfer of the contacted cell as compared to the
CC control cell is indicative of clostridial toxin activity. (M1) is useful
CC for determining clostridial toxin activity, where the sample is a crude
CC cell lysate, isolated clostridial toxin, formulated clostridial toxin
CC product, BOTOX or food. (M1) is an automated high-throughput assay. (M1)
CC reduces the need for animal toxicity studies and serves to analyze
CC multiple toxin functions such as binding a cellular uptake of the toxin,
CC translocation into the cell cytosol and protease activity. In the method
CC M1, the clostridial toxin substrate is a botulinum toxin substrate
CC selected from a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G
CC or TONT substrate comprising a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E,
CC BONT/F, BONT/G or TONT recognition sequence. This sequence corresponds to
CC a recognition sequence for a botulinum toxin used as the clostridial
CC toxin substrate.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 59; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIDEANORATKM 12
 DB 5 RIDEANORATKM 16

RESULT 13
 ADM97061
 ID ADM97061 standard; peptide; 16 AA.
 XX
 AC ADM97061;
 DT 01-JUL-2004 (first entry)
 XX Botulinum toxin substrate recognition sequence #46.
 XX clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.
 DE
 KW clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.
 XX Synthetic.
 OS
 XX WO2004029576-A2.
 PN
 XX 08-APR-2004.
 PD
 XX 04-SEP-2003; 2003WO-US028092.
 PF
 XX 27-SEP-2002; 2002US-00261161.
 PR
 XX (ALLR) ALLERGAN INC.
 PA
 XX Fernandez-Salas E, Steward LE, Aoki KR;
 PI
 XX WPI; 2004-340456/31.
 DR
 XX Determining clostridial toxin activity, comprises contacting cell with
 PT sample comprising substrate with donor fluorophore, acceptor and
 PT recognition sequence, exciting fluorophore, and determining resonance
 PT energy transfer of contacted cell.
 PT
 XX Disclosure; SEQ ID NO 67; 188pp; English.

The invention relates to a method of determining (M1) clostridial toxin activity, comprising contacting cell with sample comprising clostridial toxin substrate with donor fluorophore (F), acceptor (A) with an absorbance spectrum overlapping emission spectrum of fluorophore clostridial toxin recognition sequence with cleavage site intervening between (F) and (A), where under appropriate conditions resonance transfer is exhibited between fluorophore and acceptor, exciting the donor fluorophore, and determining resonance energy transfer of the contacted cell relative to a control cell, where a difference in resonance energy transfer of the contacted cell as compared to the control cell is indicative of clostridial toxin activity. (M1) is useful for determining clostridial toxin activity, where the sample is a crude cell lysate, isolated clostridial toxin, formulated clostridial toxin product, BOTOX or food. (M1) is an automated high-throughput assay. (M1) reduces the need for animal toxicity studies and serves to analyze multiple toxin functions such as binding a cellular uptake of the toxin, translocation into the cell cytosol and protease activity. In the method M1, the clostridial toxin substrate is a botulinum toxin substrate selected from a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G or TeNT substrate comprising a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G or TeNT recognition sequence. This sequence corresponds to a recognition sequence for a botulinum toxin used as the clostridial toxin substrate.

XX Sequence 16 AA;
 Query Match 100.0%; Score 59; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00027;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIDEANORATKM 12
 DB 5 RIDEANORATKM 16

RESULT 15
 AAY44057
 ID AAY44057 standard; peptide; 17 AA.
 XX
 AC AAY44057;
 DT 18-JAN-2000 (first entry)
 XX Human SNAP25 (amino acids 187-203) analogue #36.
 DE Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;
 KW fluorescamine; detection; human; synaptosomal protein; SNAP25;
 KW

DB 5 RIDEANORATKM 16

RESULT 14
 AEAL4919
 ID AEAL4919 standard; peptide; 16 AA.
 XX
 AC AEAL4919;
 DT 14-JUL-2005 (first entry)
 XX Human SNAP-25 substrate BONT/A recognition sequence, SEQ ID NO: 29.
 DE Neurotoxin; fluorescence; SNAP-25; botulinum toxin.
 KW Neurotoxin; fluorescence; SNAP-25; botulinum toxin.
 XX Homo sapiens.
 OS
 XX US2005100973-A1.
 PN
 XX 12-MAY-2005.
 PD
 XX 13-AUG-2004; 2004US-00917844.
 PF
 XX 28-AUG-2001; 2001US-00942098.
 PR
 XX (ALLR) ALLERGAN SALES INC.
 PA
 XX Steward LE, Gilmore MA, Aoki KR;
 PI
 XX WPI; 2005-365632/37.
 DR
 XX Determining clostridial toxin protease activity, by treating sample with
 PT tagged toxin substrate comprising fluorescent protein, first and second
 PT partner of affinity couple and assaying fluorescent cleavage product in
 PT treated sample.
 PT
 XX Disclosure; SEQ ID NO 29; 97pp; English.

The present invention relates to a method for determining protease activity of clostridial neurotoxins such as botulinum neurotoxin (BoNT) and tetanus neurotoxin (TeNT). The method involves treating with a sample, in solution phase under conditions suitable for clostridial toxin protease activity, a tagged toxin substrate (e.g. SNAP-25, VAMP, syntaxin) comprising fluorescent protein, first partner of affinity couple and clostridial toxin recognition sequence comprising cleavage site; contacting treated sample with second partner of affinity couple; and assaying presence of fluorescent cleavage product in the treated sample. The present sequence is the human SNAP-25 substrate BONT/A (botulinum neurotoxin serotype A) recognition sequence.

XX Sequence 16 AA;
 Query Match 100.0%; Score 59; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00027;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIDEANORATKM 12
 DB 5 RIDEANORATKM 16

RESULT 15
 AAY44057
 ID AAY44057 standard; peptide; 17 AA.
 XX
 AC AAY44057;
 DT 18-JAN-2000 (first entry)
 XX Human SNAP25 (amino acids 187-203) analogue #36.
 DE Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;
 KW fluorescamine; detection; human; synaptosomal protein; SNAP25;
 KW

KW hydrolysis; amino group.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US5965699-A.
XX
XX 12-OCT-1999.
PD
XX
XX 06-NOV-1996; 96US-00743894.
PF
XX
XX 06-NOV-1996; 96US-00743894.
PR
XX
XX (USSA) US SEC OF ARMY.
PA
XX
XX Bostian KA, Schmidt JJ;
PI
XX
XX WPI; 1999-579939/49.
DR
XX
XX Quantitation of type A botulinum toxin.
PT
XX
XX Disclosure; Col 9; 28pp; English.
PS
XX
XX The invention relates to an enzymatic assay for the quantitation of type
CC A botulinum toxin, by determining the proteolytic activity of botulinum
CC neurotoxin type A using fluorescamine detection. Botulinum toxin A has
CC been shown to cleave the synaptosomal neurotransmitter peptide SNAP25
CC between residues 197-198. The method comprises adding an analogue (e.g.
CC AAY4022-Y44076) of the SNAP25 peptide (AAY44021, amino acids 187-203 of
CC human SNAP25) to a sample containing the botulinum toxin A so that
CC hydrolysis of the peptide is initiated, then stopping hydrolysis of the
CC peptide at different time points; and measuring the amount of hydrolysis
CC at each time point by combining with a label capable of detecting free
CC amino groups resulting from the hydrolysis. The amount of botulinum toxin
CC A present in the sample is determined by comparing measurements with the
CC amount of label produced from a known concentration of toxin measured
CC under similar conditions. The method is useful for the quantitation of
CC type A botulinum toxin
XX
XX Sequence 17 AA;

Query Match 100.0%; Score 59; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIDEANQRATKM 12
| | | | | | | | | |
Db 5 RIDEANQRATKM 16

Search completed: April 3, 2006, 15:36:56
Job time : 61.708 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:49:32 ; Search time 8.51376 Seconds
(without alignments)
57.210 Million cell updates/sec

Title: US-09-942-098-29

Perfect score: 79

Sequence: 1 SNKTRIDEANQRATKM 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pep.*
- 2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep.*
- 3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep.*
- 4: /SIDSS/ptodata/1/pubpaa/PTCT_NEW PUB.pep.*
- 5: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pep.*
- 6: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep.*
- 7: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep.*
- 8: /SIDSS/ptodata/1/pubpaa/US60_NEW PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	79	100.0	16	US-10-947-071-32
2	79	100.0	16	US-10-948-097-32
3	79	100.0	17	US-10-980-346B-6
4	79	100.0	17	US-10-980-346B-37
5	79	100.0	17	US-10-947-071-33
6	79	100.0	17	US-10-947-071-34
7	79	100.0	17	US-10-948-097-33
8	79	100.0	17	US-10-948-097-34
9	79	100.0	18	US-10-947-071-35
10	79	100.0	18	US-10-948-097-35
11	79	100.0	33	US-10-947-071-36
12	79	100.0	33	US-10-947-071-40
13	79	100.0	33	US-10-947-071-41
14	79	100.0	33	US-10-948-097-36
15	79	100.0	33	US-10-948-097-40
16	79	100.0	33	US-10-948-097-41
17	79	100.0	116	US-11-195-098-11
18	79	100.0	203	US-10-947-071-4
19	79	100.0	203	US-10-948-097-4
20	79	100.0	206	US-10-947-071-1
21	79	100.0	206	US-10-947-071-2
22	79	100.0	206	US-10-948-097-1
23	79	100.0	206	US-10-948-097-2
24	79	100.0	206	US-11-169-041-225
25	79	100.0	334	US-10-947-071-20

26	79	100.0	334	6	US-10-948-097-20	Sequence 20, Appl
27	76	96.2	17	6	US-10-947-071-61	Sequence 61, Appl
28	76	96.2	17	6	US-10-948-097-61	Sequence 61, Appl
29	75	94.9	17	6	US-10-947-071-53	Sequence 53, Appl
30	75	94.9	17	6	US-10-947-071-55	Sequence 55, Appl
31	75	94.9	17	6	US-10-947-071-60	Sequence 60, Appl
32	75	94.9	17	6	US-10-948-097-53	Sequence 53, Appl
33	75	94.9	17	6	US-10-948-097-55	Sequence 55, Appl
34	75	94.9	17	6	US-10-948-097-60	Sequence 60, Appl
35	74	93.7	15	6	US-10-947-071-31	Sequence 31, Appl
36	74	93.7	15	6	US-10-948-097-31	Sequence 31, Appl
37	74	93.7	17	6	US-10-947-071-50	Sequence 50, Appl
38	74	93.7	17	6	US-10-947-071-51	Sequence 51, Appl
39	74	93.7	17	6	US-10-947-071-54	Sequence 54, Appl
40	74	93.7	17	6	US-10-947-071-58	Sequence 58, Appl
41	74	93.7	17	6	US-10-947-071-62	Sequence 62, Appl
42	74	93.7	17	6	US-10-948-097-50	Sequence 50, Appl
43	74	93.7	17	6	US-10-948-097-51	Sequence 51, Appl
44	74	93.7	17	6	US-10-948-097-54	Sequence 54, Appl
45	74	93.7	17	6	US-10-948-097-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-10-947-071-32
; Sequence 32, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-32

Query Match 100.0%; Score 79; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 1 SNKTRIDEANQRATKM 16

RESULT 2
US-10-948-097-32
; Sequence 32, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-32

Query Match          100.0%; Score 79; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKM 16
Db 1 SNKTRIDEANQRATKM 16

RESULT 3
US-10-980-346B-6
; Sequence 6, Application US/10980346B
; Publication No. US20060024763A1
; GENERAL INFORMATION:
; APPLICANT: Los Alamos National Laboratory
; APPLICANT: Schmidt, Jurgen G., et al.
; TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
; FILE REFERENCE: S-102,313
; CURRENT APPLICATION NUMBER: US/10/980,346B
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum
; OTHER INFORMATION: Neurotoxin (BoNT)
US-10-980-346B-6

Query Match          100.0%; Score 79; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKM 16
Db 1 SNKTRIDEANQRATKM 16

RESULT 4
US-10-980-346B-37
; Sequence 37, Application US/10980346B
; Publication No. US20060024763A1
; GENERAL INFORMATION:
; APPLICANT: Los Alamos National Laboratory
; APPLICANT: Schmidt, Jurgen G., et al.
; TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation
; FILE REFERENCE: S-102,313
; CURRENT APPLICATION NUMBER: US/10/980,346B
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum
; OTHER INFORMATION: Neurotoxin (BoNT)
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(17)
; OTHER INFORMATION: amide bound at one end of the peptide
```

```
US-10-980-346B-37

Query Match          100.0%; Score 79; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKM 16
Db 1 SNKTRIDEANQRATKM 16

RESULT 5
US-10-947-071-33
; Sequence 33, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-33

Query Match          100.0%; Score 79; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKM 16
Db 1 SNKTRIDEANQRATKM 16

RESULT 6
US-10-947-071-34
; Sequence 34, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-34

Query Match          100.0%; Score 79; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKM 16
Db 2 SNKTRIDEANQRATKM 17
```

```

; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-35

Query Match      100.0%; Score 79; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKM 16
Db      2 SNKTRIDEANQRATKM 17

RESULT 10
US-10-948-097-35
; Sequence 35, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-35

Query Match      100.0%; Score 79; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKM 16
Db      2 SNKTRIDEANQRATKM 17

RESULT 11
US-10-947-071-36
; Sequence 36, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-34

Query Match      100.0%; Score 79; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKM 16
Db      1 SNKTRIDEANQRATKM 16

RESULT 8
US-10-948-097-34
; Sequence 34, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-33

Query Match      100.0%; Score 79; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKM 16
Db      2 SNKTRIDEANQRATKM 17

RESULT 9
US-10-947-071-35
; Sequence 35, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-33

```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-947-071-36

Query Match      100.0%; Score 79; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKM 16
Db      14 SNKTRIDEANQRATKM 29

RESULT 12
US-10-947-071-40
; Sequence 41, Application US/10947071
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-40

Query Match      100.0%; Score 79; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKM 16
Db      14 SNKTRIDEANQRATKM 29

RESULT 13
US-10-947-071-41
; Sequence 41, Application US/10947071
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-41

Query Match      100.0%; Score 79; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKM 16
Db      14 SNKTRIDEANQRATKM 29

RESULT 14
US-10-948-097-36
; Sequence 36, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-948-097-36

Query Match      100.0%; Score 79; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKM 16
Db      14 SNKTRIDEANQRATKM 29

RESULT 15
US-10-948-097-40
; Sequence 40, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-40

Query Match      100.0%; Score 79; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNKTRIDEANQRATKM 16
Db      14 SNKTRIDEANQRATKM 29

Search completed: April 3, 2006, 15:58:09
Job time : 8.51376 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:46:49 ; Search time 68.844 Seconds
(without alignments)
97.107 Million cell updates/sec

Title: US-09-942-098-29

Perfect score: 79

Sequence: 1 SNKTRIDEANQRATKM 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

1: /cgm2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
2: /cgm2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
3: /cgm2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
4: /cgm2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
5: /cgm2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
6: /cgm2_6/ptodata/1/pubaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	16	3	US-09-942-024-29
2	79	100.0	16	3	US-09-942-098-29
3	79	100.0	16	4	US-10-261-161-51
4	79	100.0	16	4	US-10-261-161-67
5	79	100.0	16	5	US-09-917-844-29
6	79	100.0	17	3	US-09-942-024-30
7	79	100.0	17	3	US-09-942-024-31
8	79	100.0	17	3	US-09-942-098-30
9	79	100.0	17	3	US-09-942-098-31
10	79	100.0	17	4	US-10-011-588-2
11	79	100.0	17	4	US-10-261-161-52
12	79	100.0	17	4	US-10-261-161-53
13	79	100.0	17	4	US-10-261-161-68
14	79	100.0	17	5	US-10-261-161-69
15	79	100.0	17	5	US-10-917-844-30
16	79	100.0	18	3	US-09-942-024-32
17	79	100.0	18	3	US-09-942-098-32
18	79	100.0	18	4	US-10-261-161-54
19	79	100.0	18	5	US-10-917-844-32
20	79	100.0	19	4	US-10-705-857-6
21	79	100.0	21	3	US-09-942-024-89
22	79	100.0	21	3	US-09-942-098-89
23	79	100.0	23	3	US-09-942-024-88
24	79	100.0	23	3	US-09-942-098-88
25	79	100.0	24	3	US-09-942-024-90
26	79	100.0	24	3	US-09-942-098-90
27	79	100.0	33	3	US-09-942-024-33

```

28 79 100.0 33 3 US-09-942-024-37 Sequence 17, Appl
29 79 100.0 33 3 US-09-942-024-38 Sequence 38, Appl
30 79 100.0 33 3 US-09-942-098-33 Sequence 33, Appl
31 79 100.0 33 3 US-09-942-098-37 Sequence 37, Appl
32 79 100.0 33 3 US-09-942-098-38 Sequence 38, Appl
33 79 100.0 33 4 US-10-261-161-55 Sequence 55, Appl
34 79 100.0 33 4 US-10-261-161-59 Sequence 59, Appl
35 79 100.0 33 4 US-10-261-161-60 Sequence 60, Appl
36 79 100.0 33 5 US-10-917-844-33 Sequence 33, Appl
37 79 100.0 33 5 US-10-917-844-37 Sequence 37, Appl
38 79 100.0 33 5 US-10-917-844-38 Sequence 38, Appl
39 79 100.0 86 4 US-10-705-857-4 Sequence 4, Appl
40 79 100.0 114 5 US-10-917-844-112 Sequence 112, App
41 79 100.0 116 3 US-09-962-360B-11 Sequence 11, Appl
42 79 100.0 116 4 US-10-802-574-11 Sequence 11, Appl
43 79 100.0 203 3 US-09-942-024-14 Sequence 14, Appl
44 79 100.0 203 3 US-09-942-098-14 Sequence 14, Appl
45 79 100.0 203 4 US-10-261-161-7 Sequence 7, Appl

```

ALIGNMENTS

```

RESULT 1
US-09-942-024-29
; Sequence 29, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-29

```

```

Query Match 100.0%; Score 79; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 SNKTRIDEANQRATKM 16
|||||
Db 1 SNKTRIDEANQRATKM 16
|||||

```

```

RESULT 2
US-09-942-098-29
; Sequence 29, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-29

```

Query Match 100.0%; Score 79; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 1 SNKTRIDEANQRATKM 16

RESULT 3

US-10-261-161-51
; Sequence 51, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261.161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-51

Query Match 100.0%; Score 79; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 1 SNKTRIDEANQRATKM 16

RESULT 4

US-10-261-161-67
; Sequence 67, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261.161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-261-161-67

Query Match 100.0%; Score 79; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 1 SNKTRIDEANQRATKM 16

RESULT 5

US-10-917-844-29
; Sequence 29, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
; APPLICANT: Aoki, Kei R.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
; FILE REFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917.844
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-844-29

Query Match 100.0%; Score 79; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 1 SNKTRIDEANQRATKM 16

RESULT 6

US-09-942-024-30
; Sequence 30, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: FRET Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-30

Query Match 100.0%; Score 79; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 1 SNKTRIDEANQRATKM 16

RESULT 7

US-09-942-024-31
; Sequence 31, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: FRET Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024

; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-31

Query Match 100.0%; Score 79; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKM 16
| | | | | | | | | | | | | | | | | | | |
Db 2 SNKTRIDEANORATKM 17

RESULT 8

US-09-942-098-30
; Sequence 30, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-30

Query Match 100.0%; Score 79; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKM 16
| | | | | | | | | | | | | | | | | | | |
Db 1 SNKTRIDEANORATKM 16

RESULT 9

US-09-942-098-31
; Sequence 31, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-31

Query Match 100.0%; Score 79; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKM 16
| | | | | | | | | | | | | | | | | | | |
Db 2 SNKTRIDEANORATKM 17

RESULT 10

US-10-011-588-2
; Sequence 2, Application US/10011588
; Publication No. US20020168727A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Leonard
; APPLICANT: Jensen, Melody
; TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS AND LIGHT CHAIN FUSION PROTEINS FOR USE IN
; TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY
; FILE REFERENCE: A34796 067252.0113
; CURRENT APPLICATION NUMBER: US/10/011,588
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 09/910,186
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/611,419
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 60/246,744
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 60/311,966
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: Residues 187-203 of SNAP-25
US-10-011-588-2

Query Match 100.0%; Score 79; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKM 16
| | | | | | | | | | | | | | | | | | | |
Db 1 SNKTRIDEANORATKM 16

RESULT 11

US-10-261-161-52
; Sequence 52, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-52

Query Match 100.0%; Score 79; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKM 16

```
Db 1 SNKTRIDEANQRATKM 16
|||||
RESULT 12
US-10-261-161-53
; Sequence 53, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-53

Query Match 100.0%; Score 79; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 2 SNKTRIDEANQRATKM 17
|||||

RESULT 13
US-10-261-161-68
; Sequence 68, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-261-161-68

Query Match 100.0%; Score 79; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 1 SNKTRIDEANQRATKM 16
|||||

RESULT 14
US-10-917-844-30
; Sequence 30, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
; APPLICANT: Aoki, Kei R.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
; FILE REFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917,844
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-844-30

Query Match 100.0%; Score 79; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 2 SNKTRIDEANQRATKM 17
|||||

RESULT 15
US-10-917-844-31
; Sequence 31, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
; APPLICANT: Aoki, Kei R.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
; FILE REFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917,844
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-844-31

Query Match 100.0%; Score 79; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 2 SNKTRIDEANQRATKM 17
|||||

Search completed: April 3, 2006, 15:57:05
Job time : 68.844 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM protein - protein search, using sw model

Run on: April 3, 2006, 15:31:39 ; Search time 12.7706 Seconds
(without alignments)
103.582 Million cell updates/sec

Title: US-09-942-098-29

Perfect score: 79

Sequence: 1 SNKTRIDEANQRATKM 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5 COMB.pdp.*

2: /cgn2_6/ptodata/1/iaa/6 COMB.pdp.*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pdp.*

4: /cgn2_6/ptodata/1/iaa/PCRU COMB.pdp.*

5: /cgn2_6/ptodata/1/iaa/RE COMB.pdp.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	16	1	US-08-743-894B-49
2	79	100.0	17	1	US-08-743-894B-1
3	79	100.0	17	1	US-08-743-894B-37
4	79	100.0	20	2	US-08-819-286-9
5	79	100.0	26	2	US-08-819-286-8
6	79	100.0	37	2	US-08-819-286-4
7	79	100.0	70	1	US-08-760-001-10
8	79	100.0	70	2	US-09-015-960-10
9	79	100.0	70	2	US-09-534-572-10
10	79	100.0	116	2	US-09-962-360B-11
11	79	100.0	206	1	US-08-393-985-18
12	79	100.0	206	2	US-08-819-286-1
13	79	100.0	206	2	US-09-949-016-6311
14	79	100.0	219	2	US-09-949-016-10671
15	76	96.2	17	1	US-08-743-894B-18
16	76	96.2	17	1	US-08-743-894B-43
17	75	94.9	17	1	US-08-743-894B-27
18	75	94.9	17	1	US-08-743-894B-30
19	75	94.9	17	1	US-08-743-894B-32
20	75	94.9	17	1	US-08-743-894B-39
21	74	93.7	15	1	US-08-743-894B-38
22	74	93.7	17	1	US-08-743-894B-19
23	74	93.7	17	1	US-08-743-894B-24
24	74	93.7	17	1	US-08-743-894B-25
25	74	93.7	17	1	US-08-743-894B-28
26	74	93.7	17	1	US-08-743-894B-29
27	74	93.7	17	1	US-08-743-894B-42

Sequence 50, Appl
Sequence 51, Appl
Sequence 2, Appl
Sequence 20, Appl
Sequence 26, Appl
Sequence 31, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 36, Appl
Sequence 44, Appl
Sequence 45, Appl
Sequence 46, Appl
Sequence 8, Appl
Sequence 12, Appl
Sequence 21, Appl
Sequence 35, Appl
Sequence 47, Appl
Sequence 48, Appl

74 93.7 17 1 US-08-743-894B-50
73 92.4 16 1 US-08-743-894B-51
73 92.4 17 1 US-08-743-894B-2
73 92.4 17 1 US-08-743-894B-20
73 92.4 17 1 US-08-743-894B-26
73 92.4 17 1 US-08-743-894B-31
73 92.4 17 1 US-08-743-894B-33
73 92.4 17 1 US-08-743-894B-34
73 92.4 17 1 US-08-743-894B-36
73 92.4 17 1 US-08-743-894B-44
73 92.4 17 1 US-08-743-894B-45
73 92.4 17 1 US-08-743-894B-46
73 92.4 24 2 US-09-962-360B-8
73 92.4 116 2 US-08-743-894B-12
71 89.9 17 1 US-08-743-894B-21
71 89.9 17 1 US-08-743-894B-35
71 89.9 17 1 US-08-743-894B-47
71 89.9 17 1 US-08-743-894B-48

ALIGNMENTS

RESULT 1

US-08-743-894B-49

; Sequence 49, Application US/08743894B

; Patent No. 5965699

; GENERAL INFORMATION:

; APPLICANT: James J. Schmidt

; APPLICANT: Karen A. Bostian

; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty

; STREET: USA MEMC - 504 Scott Street

; CITY: FORT DETRICK

; STATE: MARYLAND

; COUNTRY: USA

; ZIP: 21702-5012

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 7.0

; SOFTWARE: Microsoft Word 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/743.894B

; FILING DATE: No. 5965699ember 6, 1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Charles H. Harris

; REGISTRATION NUMBER: 34,616

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 619-2065

; TELEFAX: (301) 619-7714

; INFORMATION FOR SEQ ID NO: 49:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: amino acid sequence

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; FEATURE:

; US-08-743-894B-49

Query Match 100.0%; Score 79; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.4e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SNKTRIDEANQRATKM 16

|||||

Db 1 SNKTRIDEANORATKM 16

RESULT 2

US-08-743-894B-1
Sequence 1, Application US/08743894B

Patent No. 5965699

GENERAL INFORMATION:

APPLICANT: James J. Schmidt

APPLICANT: Karen A. Bostian

TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty

STREET: USA MMC - 504 Scott Street

CITY: FORT DETRICK

STATE: MARYLAND

COUNTRY: USA

ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/743,894B

FILING DATE: No. 5965699ember 6, 1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Charles H. Harris

REGISTRATION NUMBER: 34,616

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 619-2065

TELEFAX: (301) 619-7714

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid sequence

STRANDEDNESS: Single

TOPOLOGY: Linear

US-08-743-894B-1

Query Match 100.0%; Score 79; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKM 16

Db 1 SNKTRIDEANORATKM 16

RESULT 3

US-08-743-894B-37

Sequence 37, Application US/08743894B

Patent No. 5965699

GENERAL INFORMATION:

APPLICANT: James J. Schmidt

APPLICANT: Karen A. Bostian

TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty

STREET: USA MMC - 504 Scott Street

CITY: FORT DETRICK

STATE: MARYLAND

COUNTRY: USA

ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/743,894B

FILING DATE: No. 5965699ember 6, 1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Charles H. Harris

REGISTRATION NUMBER: 34,616

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 619-2065

TELEFAX: (301) 619-7714

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid sequence

STRANDEDNESS: Single

TOPOLOGY: Linear

FEATURE:

US-08-743-894B-37

Query Match 100.0%; Score 79; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKM 16

Db 1 SNKTRIDEANORATKM 16

RESULT 4

US-08-819-286-9

Sequence 9, Application US/08819286

Patent No. 6163074

GENERAL INFORMATION:

APPLICANT: Montal, Mauricio

TITLE OF INVENTION: PEPTIDE INHIBITORS OF

TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/819,286

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/013,599

FILING DATE: 18-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Taylor, Stacy L.

REGISTRATION NUMBER: 34,842

REFERENCE/DOCKET NUMBER: 07349/005001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

```

; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-9
Query Match 100.0%; Score 79; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 1 SNKTRIDEANQRATKM 16

RESULT 5
US-08-819-286-8
; Sequence 8, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-4

Query Match 100.0%; Score 79; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 18 SNKTRIDEANQRATKM 33

RESULT 7
US-08-760-001-10
; Sequence 10, Application US/08760001
; Patent No. 5962637
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,001

```

```
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA: PCT/GB95/01279
; APPLICATION NUMBER: 02-JUN-1995
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-760-001-10
Query Match 100.0%; Score 79; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 51 SNKTRIDEANQRATKM 66

RESULT 8
US-09-015-960-10
; Sequence 10, Application US/09015960
; Patent No. 6043042
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,960
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,960
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE: 30-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-015-960-10
Query Match 100.0%; Score 79; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 51 SNKTRIDEANQRATKM 66
```

```
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA: PCT/GB95/01279
; APPLICATION NUMBER: 02-JUN-1995
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-015-960-10
Query Match 100.0%; Score 79; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 51 SNKTRIDEANQRATKM 66

RESULT 9
US-09-534-572-10
; Sequence 10, Application US/09534572
; Patent No. 6337386
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,572
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,960
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE: 30-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-534-572-10
Query Match 100.0%; Score 79; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 51 SNKTRIDEANQRATKM 66
```

```
RESULT 10
US-09-962-360B-11
; Sequence 11, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962.360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-09-962-360B-11

Query Match 100.0%; Score 79; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.4e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 96 SNKTRIDEANQRATKM 111

RESULT 11
US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Scheller, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids

Query Match 100.0%; Score 79; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.4e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 96 SNKTRIDEANQRATKM 111

RESULT 12
US-08-819-286-1
; Sequence 1, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-1

Query Match 100.0%; Score 79; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.6e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 187 SNKTRIDEANQRATKM 202

RESULT 13
US-09-949-016-6311
; Sequence 6311, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
```

```
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-393-985-18

Query Match 100.0%; Score 79; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.6e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 187 SNKTRIDEANQRATKM 202

RESULT 12
US-08-819-286-1
; Sequence 1, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-1

Query Match 100.0%; Score 79; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.6e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 187 SNKTRIDEANQRATKM 202

RESULT 13
US-09-949-016-6311
; Sequence 6311, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:27:42 ; Search time 82.4954 Seconds
(without alignments)
136.837 Million cell updates/sec

Title: US-09-942-098-29
Perfect score: 79
Sequence: 1 SNKTRIDEANQRATKM 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	79	100.0	124	2	O93578_BRARE	O93578 brachydanio
2	79	100.0	134	2	O488B5_TETNG	O488b5 tetraodon n
3	79	100.0	143	2	Q9GM34_MACFA	Q9gm34 macaca fasc
4	79	100.0	198	2	Q6PC84_BRARE	Q6pc84 brachydanio
5	79	100.0	203	1	SN25B_CARAU	P36978 carassius a
6	79	100.0	203	2	O93579_BRARE	O93579 brachydanio
7	79	100.0	203	2	Q6PC54_BRARE	O6pc54 brachydanio
8	79	100.0	204	1	SN25A_CARAU	P36977 carassius a
9	79	100.0	204	2	Q705J6_LATJA	Q705j6 lateolabrax
10	79	100.0	204	2	Q5TZ66_BRARE	Q5tz66 brachydanio
11	79	100.0	204	2	Q5TZ65_BRARE	Q5tz65 brachydanio
12	79	100.0	206	1	SNP25_CHICK	P60878 gallus gall
13	79	100.0	206	1	SNP25_HUMAN	P60880 homo sapien
14	79	100.0	206	1	SNP25_MACMU	P60877 macaca mula
15	79	100.0	206	1	SNP25_MOUSE	P60879 mus musculus
16	79	100.0	206	1	SNP25_PANTR	Q5rix1 pan troglod
17	79	100.0	206	1	SNP25_RAT	P60881 rattus norv
18	79	100.0	206	2	Q5JEM2_HUMAN	Q5jem2 homo sapien
19	79	100.0	206	2	Q5U0B5_HUMAN	Q5u0b5 homo sapien
20	79	100.0	206	2	Q5NVG5_PONPY	Q5nvgs pongo pygma
21	79	100.0	206	2	Q5NVK3_PONPY	Q5nvk3 pongo pygma
22	79	100.0	206	2	Q5R690_PONPY	Q5r690 pongo pygma
23	79	100.0	206	2	Q5R6U7_PONPY	Q5r6u7 pongo pygma
24	79	100.0	206	2	Q4R4U6_MACFA	Q4r4u6 macaca fasc
25	79	100.0	236	2	Q4VS09_CARAU	Q4vs09 carassius a
26	75	94.9	204	2	Q6P3L7_BRARE	Q6p3l7 brachydanio
27	72	91.1	206	2	Q5R505_PONPY	Q5r505 pongo pygma
28	65	82.3	206	2	Q640W4_XENLA	Q640w4 xenopus lae
29	65	82.3	206	2	Q8AXM1_XENLA	Q8axm1 xenopus lae
30	65	82.3	206	2	Q8AXM2_XENLA	Q8axm2 xenopus lae
31	62	78.5	214	2	Q7ZVE4_BRARE	Q7zve4 brachydanio

32	62	78.5	230	2	Q4REP6_TETNG	Q4rep6 tetraodon n
33	61	77.2	210	1	SNP25_TORMA	P36976 torpido mar
34	61	77.2	212	2	Q8T3S4_LOLPE	Q8t3s4 loligo peal
35	59	74.7	137	2	Q66ID7_BRARE	Q66id7 brachydanio
36	59	74.7	186	2	Q4V9B7_BRARE	Q4v9b7 brachydanio
37	59	74.7	209	2	Q4V9B6_BRARE	Q4v9b6 brachydanio
38	58	73.4	204	2	Q8JIS7_XENLA	O8jis7 xenopus lae
39	49	62.0	212	2	O01389_HIRME	O01389 hirudo medi
40	48	60.8	210	1	SNP23_MOUSE	O09044 mus musculus
41	48	60.8	210	1	SNP23_RAT	O70377 rattus norv
42	48	60.8	221	2	Q9D3L3_MOUSE	O9d3l3 mus musculus
43	47	59.5	211	2	Q5R5T6_PONPY	O5r5t6 pongo pygma
44	44	55.7	191	2	Q8ZV72_PYRAE	O8zv72 pyrobaculum
45	44	55.7	211	1	SNP23_HUMAN	O00161 homo sapien

ALIGNMENTS

RESULT 1
O93578_BRARE
ID O93578_BRARE PRELIMINARY; PRT; 124 AA.
AC O93578; 1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Synaptosome-associated protein 25.1 (Fragment).
GN Name=snap25a; Synonyms=Snap;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9057281; Pubmed=9843147;
RX DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNRL13.3.CO;2-Z;
RA Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
RA Larhammar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish:
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage.";
RL J. Neurosci. Res. 54:563-573(1998).
DR EMBL; AF091593; AAC64289.1; -; mRNA.
DR HSSP; Q8T3S4; 1L4A.
DR SRR; Q93578; 49-122.
DR Ensembl; ENSDARG0000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR GO; GO:0019717; C:synaptosome; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002197; HTH_Fis.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR PRINTS; PR01590; HTHFIS.
DR SMART; SM00397; t-SNARE; 1.
DR PROSITE; PS00192; t-SNARE; 1.
DR Synaptosome.
KW NON TER
FT
SQ SEQUENCE 124 AA; 13616 MW; 50E27DBDB33D958C CRC64;

Query Match 100.0%; Score 79; DB 2; Length 124;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SNKTRIDEANQRATKM 16

DB 105 SNKTRIDEANQRATKM 120

RESULT 2

Q4S8B5 TETNG
ID Q4S8B5_TETNG PRELIMINARY; PRT; 134 AA.
AC Q4S8B5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF14706, whole genome shotgun sequence.
GN ORFNames=GSTENG0022427001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anhouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cottolico L., Poulain J., De Berardinis V.,
RA Parra G., Lardier G., Chappelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Croliis H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RN Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG GenomeScope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC } EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC } preliminary data.
DR EMBL; CAAB01014706; GAG03117.1; -; Genomic DNA.
SQ SEQUENCE 134 AA; 14682 MW; 09109FF243890A8E CRC64;

Query Match 100.0%; Score 79; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKM 16
Db 115 SNKTRIDEANORATKM 130
|||||
115 SNKTRIDEANORATKM 130

RESULT 3
Q9GM34 MACFA PRELIMINARY; PRT; 143 AA.
ID Q9GM34 MACFA PRELIMINARY;
AC Q9GM34;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain parietal lobe;
RA Oseada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049852; BAB16738.1; -; mRNA.
DR HSSP; Q8T3S4; 1L4A.

DR SMR; Q9GM34; 68-141.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR00928; SNAP-25.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNAP; 1.
DR SMART; SM00397; t_SNARE; 1.
DR PROSITE; PS50192; t_SNARE; 1.
KW Hypothetical protein; Synaptosome.
SQ SEQUENCE 143 AA; 16043 MW; D625DBAAA0893FB0 CRC64;

Query Match 100.0%; Score 79; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKM 16
Db 124 SNKTRIDEANORATKM 139
|||||
124 SNKTRIDEANORATKM 139

RESULT 4
Q6PC84 BRARE PRELIMINARY; PRT; 198 AA.
ID Q6PC84 BRARE PRELIMINARY;
AC Q6PC84;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Snap25a protein.
GN Name=snap25a;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Chordata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
STRAIN=Wild-type; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
STRAIN=Wild-type; TISSUE=Eye;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059439; AAH59439.1; -; mRNA.
DR SMR; Q6PC84; 1-77, 123-196.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR00928; SNAP-25.
DR InterPro; IPR000727; t_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNAP; 1.
DR SMART; SM00397; t_SNARE; 1.
DR PROSITE; PS50192; t_SNARE; 2.

KW Synaptosome.
SQ SEQUENCE 198 AA; 22209 MW; 8PED5099A00E1EC0 CRC64;
Query Match 100.0%; Score 79; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKM 16
DB 179 SNKTRIDEANORATKM 194
|||||

RESULT 5
SN25B CARAU STANDARD; PRT; 203 AA.
ID SN25B CARAU
AC P36978;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptosomal-associated protein 25B (SNAP-25B).
GN Name=SNAP-B;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP NUCLEOTIDE SEQUENCE.
TX TISSUE=Retina;
RX MEDLINE=94069448; PubMed=8248151;
RA Rieger C., Larhammer D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC -!- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of the nerve terminal.
CC -!- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, and piriform cortex, anterior thalamic nuclei, pontine nuclei, and granule cells of the cerebellum.
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

EMBL; L22976; AA16538.1; -; mRNA.
PIR; I50481; I50481.
HSP; P13795; 1SPC.
SMR; P36978; 7-82, 128-201.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; t-SNARE.
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
SMART; SM00397; t-SNARE; 2.
PROSITE; PS50192; t-SNARE; 2.
Coiled coil; 19 81
DOMAIN 137 199
FT CARBOHYD 85 92 Cys-rich.
FT CARBOHYD 77 97 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 185 185 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 203 AA; 22664 MW; 8DFBEBEDB37D6D7 CRC64;

Query Match 100.0%; Score 79; DB 1; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKM 16
DB 184 SNKTRIDEANORATKM 199
|||||

RESULT 6
O93579 BRARE PRELIMINARY; PRT; 203 AA.
ID O93579;
AC O93579;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Synaptosome-associated protein 25.2.
GN Name=snap25b; Synonyms=Snap;
OS Brachydanio rerio (Zebrafish)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
TX MEDLINE=99057281; PubMed=9843147;
RX DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNRL13.3.CO;2-Z;
RA Rieger C., Salanek E., Soderberg C., Gates M., Postlethwait J.H., Larhammer D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish: comparison of paralogous linkage groups suggests loss of one locus in the mammalian lineage.";
RL J. Neurosci. Res. 54:563-573(1998).
DR EMBL; AF091594; AAC64290.1; -; mRNA.
DR HSP; P60881; 1JTH.
DR SMR; O93579; 7-82, 128-201.
ZFIN; ZDB-GENE-980526-392; snap25b.
GO; GO:0019717; C:synaptosome; IEA.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; t-SNARE.
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
SMART; SM00397; t-SNARE; 2.
PROSITE; PS50192; t-SNARE; 2.
KW Synaptosome.
SQ SEQUENCE 203 AA; 22647 MW; 93B759DDDC93F38 CRC64;

Query Match 100.0%; Score 79; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKM 16
DB 184 SNKTRIDEANORATKM 199
|||||

RESULT 7
O6PC54 BRARE PRELIMINARY; PRT; 203 AA.
ID O6PC54;
AC O6PC54;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Synaptosome-associated protein 25 b.
GN Name=snap25b;
OS Brachydanio rerio (Zebrafish)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
TX STRAIN=Wild-type; TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.N., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Shat N.K.,


```

RESULT 10
Q5T266_BRARE PRELIMINARY; PRT; 204 AA.
ID Q5T266;
AC Q5T266;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Synaptosomal-associated protein (SNAP).
GN Name=snap25a; Synonyms=OTTDARP0000005563; ORFNames=DKEYP-8F4.6-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lovell J.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Donaldson S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX465184; CAI21359.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69031.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69031.1; JOINED; Genomic DNA.
DR EMBL; BX465184; CAI21359.1; JOINED; Genomic DNA.
DR SMR; Q5T266; 7-83, 129-202.
DR Ensembl; ENSDARG0000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
KW Synaptosome.
KW SEQUENCE 204 AA; 22857 MW; B53CF5F3D1C69EA5 CRC64;
SQ
Query Match 100.0%; Score 79; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 185 SNKTRIDEANQRATKM 200

RESULT 11
Q5T265_BRARE PRELIMINARY; PRT; 204 AA.
ID Q5T265;
AC Q5T265;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Synaptosomal-associated protein (SNAP).
GN Name=snap25a; Synonyms=OTTDARP0000005569; ORFNames=DKEYP-8F4.6-002;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lovell J.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Donaldson S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX465184; CAH69032.1; -; Genomic DNA.
DR EMBL; BX470246; CAI21360.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69032.1; JOINED; Genomic DNA.

```

```

DR EMBL; BX465184; CAI21360.1; JOINED; Genomic DNA.
DR SMR; Q5T265; 7-83, 129-202.
DR Ensembl; ENSDARG0000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR SMART; SM00397; t_SNARE; 1.
DR PROSITE; PS50192; T_SNARE; 2.
KW Synaptosome.
KW SEQUENCE 204 AA; 22878 MW; FBC79AB7015AC0ED CRC64;
SQ
Query Match 100.0%; Score 79; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 185 SNKTRIDEANQRATKM 200

RESULT 12
SNP25_CHICK STANDARD; PRT; 206 AA.
ID P60878; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
AC P60878; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
DE 25 kDa protein) (Super protein) (SUP).
GN Name=SNAP25; Synonyms=SNAP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM SNAP25B).
RC STRAIN=White leghorn; TISSUE=Retina;
RX MEDLINE=91126080; PubMed=1992470;
CA Catsicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,
RA Wilson M.C.;
RT "Expression of a conserved cell-type-specific protein in nerve
RT terminals coincides with synaptogenesis."
RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS SNAP25A AND SNAP25B).
RX MEDLINE=93389738; PubMed=8377193;
RA Bark I.C.;
RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon
RT encoding distinct isoforms of the protein."
J. Mol. Biol. 233:67-76(1993).
CC -!- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion (By
CC similarity).
CC -!- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1
CC and SNAP25BP. Binds STXB6. Found in a ternary complex with STX1A
CC and VAMP8 (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60878-1, P13795-1;
CC Sequence=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60878-2, P13795-2;

```


RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 11-81 AND 141-202 IN COMPLEX
RP WITH STX1A; CPLX1 AND VAMP2, AND NMR ANALYSIS.
RX MEDLINE=21822661; PubMed=11832227; DOI=10.1016/S0896-6273(02)00583-4;
RY Chen X., Tomchick D.R., Kovrigin E., Arac D., Machius M.,
RT Suedhof T.C., Rizo J.;
RA "Three-dimensional structure of the complexin/SNARE complex.";
RL Neuron 33:397-409(2002).
CC -!- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion.
CC -!- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
CC SNAP25BP and HGS. Binds STXB96. Found in a ternary complex with
CC STX1A and VAMP8 (By similarity).
CC -!- INTERACTION:
CC Q8TUN5:HIP14; NDBXP=1; IntAct=EBI-524785; EBI-524753;
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment=isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60880-1, P13795-1;
CC Sequence=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60880-2, P13795-2;
CC Sequence=VSP_006186;
CC -!- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, and
CC piriform cortex, anterior thalamic nuclei, pontine nuclei, and
CC granule cells of the cerebellum.
CC -!- PTM: Palmitoylated (By similarity).
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; L19760; AAC37545.1; -; mRNA.
CC EMBL; L19761; AAC37546.1; -; mRNA.
CC EMBL; D21267; BAA22370.1; -; mRNA.
CC EMBL; AL023913; CAC34534.1; -; Genomic DNA.
CC EMBL; AL023913; CAC34535.1; -; Genomic DNA.
CC EMBL; AL023913; CAD56158.1; -; Genomic DNA.
CC EMBL; AL023913; CAB42860.1; -; Genomic DNA.
CC EMBL; BC010647; AAH10647.1; -; mRNA.
CC PIR; I53735; I53735.
CC PIR; I67823; I67823.
CC PDB; 1KIL; X-ray; C=11-80, D=141-203.
CC PDB; 1XTG; X-ray; B=146-204.
CC SMR; P60880; 7-83, 131-204.
CC IntAct; P60880; -.
CC Ensembl; ENSG00000132639; Homo sapiens.
CC HGNC; HGNC:11132; SNAP25.
CC H-InvDB; HIX0015639; -.
CC MIM; 600322; -.
CC GO; GO:0007269; P-neurotransmitter secretion; NAS.
CC GO; GO:0001504; P-neurotransmitter uptake; NAS.
CC GO; GO:0050796; P-regulation of insulin secretion; TAS.
CC GO; GO:0007268; P-synaptic transmission; NAS.
CC GO; GO:0016081; P-synaptic vesicle docking during exocytosis; NAS.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T_SNARE.

DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS01012; T_SNARE; 2.
KW 3D-structure; Alternative splicing; Coiled coil; Lipoprotein;
KW Palmitate; Phosphorylation; Repeat; Synaptosome.
FT DOMAIN 19 81
FT t-SNARE coiled-coil homology 1.
FT t-SNARE coiled-coil homology 2.
FT Cys-rich.
FT SITE 85 92
FT Cleavage (by BONT/E).
FT SITE 180 181
FT Phosphothreonine (By similarity).
FT MOD_RES 138 138
FT Phosphoserine (By similarity).
FT MOD_RES 187 187
FT ERIEEGMDQINKDKAEKRLTDLGKFCGLCV -> DRIVEE
FT VARSPLIC 58 89
FT GMNHINQDMKEAEKRLKGLKCCGLFI (in isoform
FT SNAP-25a).
FT /FTId=VSP_006186.
FT FT
FT HELIX 7 82
FT HELIX 142 201
FT TURN 202 202
FT SNKTRIDEANQRATKM 16
DB 187 SNKTRIDEANQRATKM 202
SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
Query Match 100.0%; Score 79; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNKTRIDEANQRATKM 16
|||||
DB 187 SNKTRIDEANQRATKM 202
|||||
RESULT 14
SNP25 MACMU STANDARD; PRT; 206 AA.
ID SNP25 MACMU STANDARD; PRT; 206 AA.
AC P60877; P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 13-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
DB 25 kDa protein).
GN Name=SNAP25;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hippocampus;
RA Jensen M.J., Smith L.A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion (By
CC similarity).
CC -!- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
CC SNAP25BP and HGS. Binds STXB96. Found in a ternary complex with
CC STX1A and VAMP8 (By similarity).
CC -!- PTM: Palmitoylated (By similarity).
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AF240770; AAF64477.1; -; mRNA.
CC SMR; P60877; 7-83, 131-204.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T_SNARE.

DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS0192; t-SNARE; 2.
KW Coiled coil; Lipoprotein; Palmitate; Phosphorylation; Repeat;
KW Synaptosome.
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 140 202 t-SNARE coiled-coil homology 2.
FT COMPBIAS 85 92 Cys-rich.
FT SITE 180 181 Cleavage (by BONT/E) (By similarity).
FT MOD RES 138 138 Phosphothreonine (By similarity).
FT MOD RES 187 187 Phosphoserine (By similarity).
FT SEQUENCE 206 AA; 23315 MW; PF02802A4CB6A6 CRC64;
Query Match 100.0%; Score 79; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNKTRIDEANORATKM 16
Db 187 SNKTRIDEANORATKM 202
RESULT 15
SNP25_MOUSE STANDARD; PRT; 206 AA.
AC P60879; F13795; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
DE 25 kDa protein) (Super protein) (SUP).
GN Name=Snap25; Synonyms=Snap;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP INTERACTION WITH SNAP25BP.
RC PubMed=10195194; DOI=10.1038/5673;
RX Ilardi J.M. Mochida S., Sheng Z.-H.;
RA "Snapin: a SNARE-associated protein implicated in synaptic
RT transmission.";
RL Nat. Neurosci. 2:119-124(1999).
[6]
RN PHOSPHORYLATION SITES THR-138 AND SER-187.
RC MEDLINE=22347237; PubMed=12459461; DOI=10.1016/S0014-5793(02)03629-3;
RX Hepp R., Cabaniols J.P., Roche P.A.;
RA "Differential phosphorylation of SNAP-25 in vivo by protein kinase C
RT and protein kinase A.";
RL FEBS Lett. 532:52-56(2002).
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion.
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
CC SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with
CC STX1A and VAMP8 (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60879-1, P13795-1;
CC Sequence=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60879-2, P13795-2;
CC Sequence=VSP_010019;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25B).
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=21363810; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C.P., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gibsi C., Godzik A., Gough J.,
RA Grimmond S., Guetincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinozaki A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25A).
RC STRAIN=C57BL/6; TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RN INTERACTION WITH SNAP25BP.
RC PubMed=10195194; DOI=10.1038/5673;
RX Ilardi J.M. Mochida S., Sheng Z.-H.;
RA "Snapin: a SNARE-associated protein implicated in synaptic
RT transmission.";
RL Nat. Neurosci. 2:119-124(1999).
[6]
RN PHOSPHORYLATION SITES THR-138 AND SER-187.
RC MEDLINE=22347237; PubMed=12459461; DOI=10.1016/S0014-5793(02)03629-3;
RX Hepp R., Cabaniols J.P., Roche P.A.;
RA "Differential phosphorylation of SNAP-25 in vivo by protein kinase C
RT and protein kinase A.";
RL FEBS Lett. 532:52-56(2002).
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion.
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
CC SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with
CC STX1A and VAMP8 (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60879-1, P13795-1;
CC Sequence=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60879-2, P13795-2;
CC Sequence=VSP_010019;

```
CC -!- PTM: Palmitoylated (By similarity).
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M22012; AAA61741.1; -; mRNA.
DR EMBL; AF483516; AAL90790.1; -; mRNA.
DR EMBL; AF483517; AAL90791.1; -; mRNA.
DR EMBL; AK078038; BAC37105.1; -; mRNA.
DR EMBL; BC018249; AAH18249.1; -; mRNA.
DR PIR; A33623; A33623.
DR PDB; 2BU0; Model; C=18-82, D=139-206.
DR SMR; P60879; 7-83, 131-204.
DR Ensembl; ENSMUSG0000027273; Mus musculus.
DR MGI; MGI-98331; Snap25.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0000149; F:SNARE binding; IDA.
DR GO; GO:0007269; P:neurotransmitter secretion; IMP.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25_1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; T-SNARE; 2.
DR 3D-structure; Alternative splicing; Coiled coil; Lipoprotein;
KW Palmitate; Phosphorylation; Repeat; Synaptosome.
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 140 202 t-SNARE coiled-coil homology 2.
FT COMPBIAS 85 92 Cys-rich.
FT SITE 180 181 Cleavage (by BONT/E) (By similarity).
FT MOD_RES 138 138 Phosphothreonine (by PKC and PKA).
FT MOD_RES 187 187 Phosphoserine (by PKC).
FT VARSPIC 58 89 ERIEGMDQINKMKAEKNTDLGKFCGLCV -- DRVVEE
FT GNNHINQDMKEAKENKLDLKGCCGLFI (in isoform
FT SNAP-25a).
FT /FTId=VSP_010019.
SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;

Query Match 100.0%; Score 79; DB 1; Length 206;
Best Local Similarity 100.0%; Pred.No. 1.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 187 SNKTRIDEANQRATKM 202

Search completed: April 3, 2006, 15:46:25
Job time : 83.4954 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:30:10 ; Search time 8.66055 Seconds
(without alignments)
177.756 Million cell updates/sec

Title: US-09-942-098-29
Perfect score: 79
Sequence: 1 SNKTRIDEANQRATKM 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	203	2 I50481	synapse protein SN
2	79	100.0	204	2 I50480	synapse protein SN
3	79	100.0	206	2 A37861	synaptosomal-assoc
4	79	100.0	206	2 I53735	nerve terminal pro
5	79	100.0	206	2 I67823	nerve terminal pro
6	79	100.0	206	2 A36223	synaptosomal-assoc
7	61	77.2	210	2 I50552	synapse protein -
8	48	60.8	210	2 JC5512	SNARE protein 23 -
9	44	55.7	211	2 JC5297	vesicle-membrane f
10	44	55.7	211	2 JC5296	vesicle-membrane f
11	42	53.2	234	2 T26553	hypothetical prote
12	42	53.2	401	2 E81436	transmembrane tran
13	42	53.2	420	2 S05062	hypothetical prote
14	42	53.2	2288	2 T29999	hypothetical prote
15	41	51.9	393	2 T32127	hypothetical prote
16	41	51.9	642	2 G90551	lipoprotein [impor
17	40	50.6	575	2 P98966	methyl-accepting c
18	39.5	50.0	1314	2 T09481	mating type silenc
19	39	49.4	243	2 T20653	hypothetical prote
20	38.5	48.7	918	2 G88545	protein F59B2.12 f
21	38.5	48.7	943	2 S31132	hypothetical prote
22	38	48.1	83	2 A33854	outer membrane lip
23	38	48.1	217	2 A47483	cysteine-rich omeg
24	38	48.1	219	2 A81996	hypothetical prote
25	38	48.1	294	2 S68784	cathepsin L - Para
26	38	48.1	414	2 T26205	hypothetical prote
27	38	48.1	465	2 T16618	hypothetical prote
28	38	48.1	586	1 C64988	probable sulfatase
29	38	48.1	586	2 B85858	probable sulfatase

30 38 48.1 586 2 H91013
31 38 48.1 643 2 T32269
32 38 48.1 869 2 H89864
33 38 48.1 1272 2 C96637
34 37 46.8 150 2 T19447
35 37 46.8 230 2 T18824
36 37 46.8 329 2 S73710
37 37 46.8 490 2 A35312
38 37 46.8 494 2 S64386
39 37 46.8 552 2 A64085
40 37 46.8 630 2 JU0271
41 37 46.8 651 2 A39372
42 37 46.8 738 2 B69863
43 37 46.8 1239 1 A32579
44 37 46.8 2427 2 T16613
45 36 45.6 60 2 S60851

ALIGNMENTS

RESULT 1

I50481
synapse protein SNAP-25 - goldfish
C:Species: Carassius auratus (goldfish)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50481
R:Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A:Reference number: A49632; MUID:94068448; PMID:8248151
A:Accession: I50481
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-203 <RIS>
A:Cross-references: UNIPROT:P36978; UNIPARC:UPI0000135B03; GB:L22976; NID:G349430; PIDN:f
C:Genetics:
A:Gene: SNAP-25

Query Match 100.0%; Score 79; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SNKTRIDEANQRATKM 16
|||

Db 184 SNKTRIDEANQRATKM 199
|||||

RESULT 2

I50480
synapse protein SNAP-25 - goldfish
C:Species: Carassius auratus (goldfish)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50480
R:Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A:Reference number: A49632; MUID:94068448; PMID:8248151
A:Accession: I50480
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-204 <RIS>
A:Cross-references: UNIPROT:P36977; UNIPARC:UPI0000135B02; GB:L22973; NID:G349426; PIDN:f
C:Genetics:
A:Gene: SNAP-25

Query Match 100.0%; Score 79; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SNKTRIDEANQRATKM 16
|||||

Db 185 SNKTRIDEANQRATKM 200
|||||

```
RESULT 3
A37861
synaptosomal-associated 25K protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
C;Accession: A37861
R;Catsicas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coincides with expression of a conserved cell-type-specific protein in nerve terminals
A;Reference number: A37861; MUID:91126080; PMID:1992470
A;Accession: A37861
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <CAT>
A;Cross-references: UNIPROT:P60878; UNIPARC:UPI0000001103; GB:M57957; NID:g212673; PIDN:
153735
Query Match 100.0%; Score 79; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKM 16
|||||
Db 187 SNKTRIDEANORATKM 202
|||||

RESULT 4
I53735
nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I53735
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A;Reference number: I53735; MUID:94156217; PMID:8112622
A;Accession: I53735
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: UNIPROT:P60880; UNIPARC:UPI0000002B3DD; GB:L19760; NID:g307425; PIDN:
153735
Query Match 100.0%; Score 79; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKM 16
|||||
Db 187 SNKTRIDEANORATKM 202
|||||

RESULT 5
I67823
nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I67823
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A;Reference number: I53735; MUID:94156217; PMID:8112622
A;Accession: I67823
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: UNIPROT:P60880; UNIPARC:UPI0000001103; GB:L19761; NID:g307427; PIDN:
153735
Query Match 100.0%; Score 79; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKM 16
|||||
Db 187 SNKTRIDEANORATKM 202
|||||
```

```
A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 79; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKM 16
|||||
Db 187 SNKTRIDEANORATKM 202
|||||

RESULT 6
A33623
synaptosomal-associated 25K protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 09-Jul-2004
C;Accession: A33623
R;Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.; V.
J. Cell Biol. 109, 3039-3052, 1989
A;Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differer
A;Reference number: A33623; MUID:90078337; PMID:2592413
A;Accession: A33623
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <OYL>
A;Cross-references: UNIPROT:P60879; UNIPARC:UPI0000001103; GB:M22012; GB:X51673; NID:g201
150552
Query Match 100.0%; Score 79; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKM 16
|||||
Db 187 SNKTRIDEANORATKM 202
|||||

RESULT 7
I50552
synapse protein - marbled electric ray
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50552
R;Risinger, C.; Blomqvist, A.G.; Lundell, I.; Lambertsson, A.; Nassel, D.; Pieribone, V.;
J. Biol. Chem. 268, 24408-24414, 1993
A;Title: Evolutionary conservation of a synaptosome-associated protein 25 kDa (SNAP-25) shc
A;Reference number: A49513; MUID:94043281; PMID:8226991
A;Accession: I50552
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-210 <RIS>
A;Cross-references: UNIPROT:P36976; UNIPARC:UPI0000135AFE; GB:L22020; NID:g431296; PIDN:
150552
Query Match 77.2%; Score 61; DB 2; Length 210;
Best Local Similarity 80.0%; Pred. No. 0.0034;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NKTRIDEANORATKM 16
|||||
Db 195 NKARIDEANKHATKM 209
|||||

RESULT 8
JC5512
SNARE protein 23 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5512
R;Araki, S.; Tamori, Y.; Kawanishi, M.; Shinoda, H.; Masugi, J.; Mori, H.; Niki, T.; Okaz
Biochem. Biophys. Res. Commun. 234, 257-262, 1997
A;Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c.
A;Reference number: JC5512; MUID:97312558; PMID:9168999
A;Accession: JC5512
```


Best Local Similarity 50.0%; Pred. No. 15;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 283 SNESLDKANRGADKM 298
|:::|:::|::|

RESULT 14

T29999
hypothetical protein ZC8.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29999
R;Latreille, P.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid ZC8.
A;Reference number: Z20719
A;Accession: T29999
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2288 <LAT>
A;Cross-references: UNIPROT:Q23081; UNIPARC:UPI000017BCE7; EMBL:U64862; PIDN:AAB52624.1;
A;Experimental source: strain Bristol N2; clone ZC8
C;Genetics:
A;Gene: CESP:ZC8.4
A;Map position: X
A;Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 1686/

Query Match 53.2%; Score 42; DB 2; Length 2288;
Best Local Similarity 57.1%; Pred. No. 95;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 KTRIDEANQRATKM 16
Db 626 KTRIDELNRRVENL 639
|:::|:::|::|

RESULT 15

T32127
hypothetical protein R07C3.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32127
R;Lamar, B.; Kramer, J.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid R07C3.
A;Reference number: Z21125
A;Accession: T32127
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-393 <LAM>
A;Cross-references: UNIPROT:O16766; UNIPARC:UPI00001642E9; EMBL:AF016686; PIDN:AAB66239.
A;Experimental source: strain Bristol N2; clone R07C3
C;Genetics:
A;Gene: CESP:R07C3.10
A;Map position: 2
A;Introns: 20/1; 350/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C32B5.10

Query Match 51.9%; Score 41; DB 2; Length 393;
Best Local Similarity 50.0%; Pred. No. 21;

Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
Db 97 AEKWKIKEENEKITKM 112
:|::|::|::|

Search completed: April 3, 2006, 15:31:22
Job time : 10.6606 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:27:08 ; Search time 82.055 Seconds
(without alignments)
85.675 Million cell updates/sec

Title: US-09-942-098-29

Perfect score: 79

Sequence: 1 SNKTRIDEANQRATKM 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	100.0	16	AAY44069	Aay44069 Human SNA
2	79	100.0	16	AEE36674	Aee36674 Human SNA
3	79	100.0	16	ABW01730	Abw01730 Human SNA
4	79	100.0	16	ADM97045	Adm97045 Botulinum
5	79	100.0	16	ADM97061	Adm97061 Botulinum
6	79	100.0	16	AEA14919	Aea14919 Human SNA
7	79	100.0	17	AAY44057	Aay44057 Human SNA
8	79	100.0	17	AAY44021	Aay44021 Amino aci
9	79	100.0	17	ABG69065	Abg69065 Human poi
10	79	100.0	17	ABG69065	Abg69065 Human SNA
11	79	100.0	17	AEE36675	Aee36675 Human SNA
12	79	100.0	17	ABW01732	Abw01732 Human SNA
13	79	100.0	17	ABW01731	Abw01731 Human SNA
14	79	100.0	17	ADM97046	Adm97046 Botulinum
15	79	100.0	17	ADM97062	Adm97062 Botulinum
16	79	100.0	17	ADM97047	Adm97047 Botulinum
17	79	100.0	17	AEA14921	Aea14921 Human SNA
18	79	100.0	17	AEA14920	Aea14920 Human SNA
19	79	100.0	18	AEE36677	Aee36677 Human SNA
20	79	100.0	18	ABW01733	Abw01733 Human SNA
21	79	100.0	18	ADM97048	Adm97048 Botulinum
22	79	100.0	18	AEA14922	Aea14922 Human SNA
23	79	100.0	19	AAE15586	Aae15586 Human SNA
24	79	100.0	19	ADP13171	Adp13171 SNAP 25 p

25	79	100.0	20	2	AAW30100	Aaw30100 Neurotran
26	79	100.0	20	7	ABW01798	Abw01798 FRET subs
27	79	100.0	21	6	AAE36734	Aae36734 FRET subs
28	79	100.0	21	7	ABW01790	Abw01790 FRET subs
29	79	100.0	23	6	AAE36733	Aae36733 FRET subs
30	79	100.0	23	7	ABW01789	Abw01789 FRET subs
31	79	100.0	24	6	AAE36735	Aae36735 FRET subs
32	79	100.0	24	7	ABW01791	Abw01791 FRET subs
33	79	100.0	26	2	AAW30099	Aaw30099 Neurotran
34	79	100.0	33	6	AAE36682	Aae36682 Goldfish
35	79	100.0	33	6	AAE36683	Aae36683 Goldfish
36	79	100.0	33	6	AAE36678	Aae36678 SNAP-25 p
37	79	100.0	33	7	ABW01739	Abw01739 Goldfish
38	79	100.0	33	7	ABW01734	Abw01734 Mouse SNA
39	79	100.0	33	7	ABW01738	Abw01738 Goldfish
40	79	100.0	33	8	ADM97054	Adm97054 Botulinum
41	79	100.0	33	8	ADM97053	Adm97053 Botulinum
42	79	100.0	33	8	ADM97049	Adm97049 Botulinum
43	79	100.0	33	9	AEA14927	Aea14927 Goldfish
44	79	100.0	33	9	AEA14923	Aea14923 SNAP-25 s
45	79	100.0	33	9	AEA14928	Aea14928 Goldfish

ALIGNMENTS

RESULT 1
AAY44069
ID AAY44069 standard; peptide; 16 AA.
XX
AC AAY44069;
XX
AC
DT 18-JAN-2000 (first entry)
XX
DE Human SNAP25 (amino acids 187-203) analogue [1-16].
XX
KW Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;
KW fluorescamine; detection; human; synaptosomal protein; SNAP25;
KW hydrolysis; amino group.
XX
OS Homo sapiens.
XX
FN US9565699-A.
XX
PD 12-OCT-1999.
XX
PF 06-NOV-1996; 96US-00743894.
XX
PR 06-NOV-1996; 96US-00743894.
XX
PA (USSA) US SEC OF ARMY.
XX
PI Bostian KA, Schmidt JJ;
XX
DR WPI; 1999-579939/49.
XX
PT Quantitation of type A botulinum toxin.
XX
PS Disclosure; Col 13-14; 28pp; English.
XX

The invention relates to an enzymatic assay for the quantitation of type A botulinum toxin, by determining the proteolytic activity of botulinum neurotoxin type A using fluorescamine detection. Botulinum toxin A has been shown to cleave the synaptosomal neurotransmitter peptide SNAP25 between residues 197-198. The method comprises adding an analogue (e.g. AAY44022-Y44076) of the SNAP25 peptide (AAY44021, amino acids 187-203 of human SNAP25) to a sample containing the botulinum toxin A so that hydrolysis of the peptide is initiated, then stopping hydrolysis of the peptide at different time points; and measuring the amount of hydrolysis at each time point by combining with a label capable of detecting free amino groups resulting from the hydrolysis. The amount of botulinum toxin A present in the sample is determined by comparing measurements with the amount of label produced from a known concentration of toxin measured

CC under similar conditions. The method is useful for the quantitation of
CC type A botulinum toxin
XX Sequence 16 AA;
SQ

Query Match 100.0%; Score 79; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRTAKM 16
DB 1 SNKTRIDEANQRTAKM 16

RESULT 2
AAE36674
ID AAE36674 standard; peptide; 16 AA.
XX
AC AAE36674;
XX
DT 07-AUG-2003 (first entry)
XX
DE Human SNAP-25 peptide #5.
XX
KW Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
KW cosmetic.
XX
OS Homo sapiens.
XX
PN WQ2003020948-A2.
XX
PD 13-MAR-2003.
XX
PF 22-AUG-2002; 2002WO-US027145.
XX
PR 28-AUG-2001; 2001US-00942024.
XX
PA (ALLR) ALLERGAN INC.
XX
PI Steward LE, Fernandez-Salas E, Aoki KR;
XX
DR WPI; 2003-290198/28.
XX
PT Botulinum serotype A/E substrate useful for assaying protease activity of
PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
PT toxin recognition sequence that includes a cleavage site.
XX
PS Disclosure; Page 40; 168pp; English.
XX

The present invention relates to novel clostridium toxin substrates. The
CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
CC which comprise a donor fluorophore, an acceptor having an absorbance
CC spectrum overlapping the emission spectrum of the donor fluorophore and a
CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
CC the cleavage site intervenes between the donor fluorophore and acceptor
CC and under the appropriate conditions, the resonance energy transfer is
CC exhibited between the donor and acceptor. Natural targets of clostridium
CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
CC of the invention are useful in assaying for the protease activity of any
CC clostridial toxin including botulinum toxins of all serotypes and tetanus
CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
CC samples, water samples, cosmetics, tissue samples and beverage or food
CC samples. They are useful to assay a sample from a human or animal, for
CC e.g., exposed to clostridial toxin or having one or more symptoms of a
CC clostridial toxin, to follow activity during production and purification
CC of clostridial toxin and to assay formulated clostridial toxin products
CC including pharmaceuticals and cosmetics. The present sequence is human
CC SNAP-25 peptide used in the invention
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 79; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRTAKM 16
DB 1 SNKTRIDEANQRTAKM 16

RESULT 3
ABW01730
ID ABW01730 standard; peptide; 16 AA.
XX
AC ABW01730;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human SNAP-25 BoNT/A recognition peptide #3.
XX
KW Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
KW human.
XX
OS Homo sapiens.
XX
PN US2003143651-A1.
XX
PD 31-JUL-2003.
XX
PF 28-AUG-2001; 2001US-00942098.
XX
PR 28-AUG-2001; 2001US-00942098.
XX
PA (STEW/) STEWARD L E.
PA (FERN/) FERNANDEZ-SALAS E.
PA (AOKI/) AOKI K R.
XX
PI Steward LE, Fernandez-Salas E, Aoki KR;
XX
DR WPI; 2003-829791/77.
XX
PT Determining clostridial toxin protease activity, by treating sample with
PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
PT sequence, under conditions which exhibit resonance energy transfer.
XX
PS Disclosure; Page 10; 0pp; English.
XX

The present invention provides clostridial toxin substrates useful in
CC assaying for the protease activity of any clostridial toxin including
CC toxins of all serotypes as well as tetanus toxins. The present sequence
CC is human SNAP-25 BoNT/A (botulinum neurotoxin serotype A) recognition
CC peptide
XX

Query Match 100.0%; Score 79; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRTAKM 16
DB 1 SNKTRIDEANQRTAKM 16

RESULT 4
ADM97045
ID ADM97045 standard; peptide; 16 AA.
XX
AC ADM97045;
XX
DT 01-JUL-2004 (first entry)
XX
DE Botulinum toxin substrate recognition sequence #30.
XX

XX clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.
XX Homo sapiens.
XX WO2004029576-A2.
XX 08-APR-2004.
XX 04-SEP-2003; 2003WO-US028092.
XX 27-SEP-2002; 2002US-00261161.
XX (ALLR) ALLERGAN INC.
XX Fernandez-Salas E, Steward LE, Aoki KR;
XX WPI; 2004-340456/31.
XX Determining clostridial toxin activity, comprises contacting cell with
XX sample comprising substrate with donor fluorophore, acceptor and
XX recognition sequence, exciting fluorophore, and determining resonance
XX energy transfer of contacted cell.
XX Disclosure; SEQ ID NO 51; 188pp; English.
XX The invention relates to a method of determining (M1) clostridial toxin
XX activity, comprising contacting cell with sample comprising clostridial
XX toxin substrate with donor fluorophore (F), acceptor (A) with an
XX absorbance spectrum overlapping emission spectrum of fluorophore
XX between (F) and (A), where under appropriate conditions resonance
XX transfer is exhibited between fluorophore and acceptor, exciting the
XX donor fluorophore, and determining resonance energy transfer of the
XX contacted cell relative to a control cell, where a difference in
XX resonance energy transfer of the contacted cell as compared to the
XX control cell is indicative of clostridial toxin activity. (M1) is useful
XX for determining clostridial toxin activity, where the sample is a crude
XX cell lysate, isolated clostridial toxin, formulated clostridial toxin
XX product, BOTOX or food. (M1) is an automated high-throughput assay. (M1)
XX reduces the need for animal toxicity studies and serves to analyze
XX multiple toxin functions such as binding a cellular uptake of the toxin,
XX translocation into the cell cytosol and protease activity. In the method
XX M1, the clostridial toxin substrate is a botulinum toxin substrate
XX selected from a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G
XX or TeNT substrate comprising a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E,
XX BONT/F, BONT/G or TeNT recognition sequence. This sequence corresponds to
XX a recognition sequence for a botulinum toxin used as the clostridial
XX toxin substrate.
XX Sequence 16 AA;
XX Query Match 100.0%; Score 79; DB 8; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 4.5e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SNKTRIDEANQRATKM 16
Db |||||
1 SNKTRIDEANQRATKM 16
RESULT 5
ADM97061
ID ADM97061 standard; peptide; 16 AA.
XX ADM97061;
XX 01-JUL-2004 (first entry)
XX Botulinum toxin substrate recognition sequence #46.
XX clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.
XX Synthetic.

XX WO2004029576-A2.
XX 08-APR-2004.
XX 04-SEP-2003; 2003WO-US028092.
XX 27-SEP-2002; 2002US-00261161.
XX (ALLR) ALLERGAN INC.
XX Fernandez-Salas E, Steward LE, Aoki KR;
XX WPI; 2004-340456/31.
XX Determining clostridial toxin activity, comprises contacting cell with
XX sample comprising substrate with donor fluorophore, acceptor and
XX recognition sequence, exciting fluorophore, and determining resonance
XX energy transfer of contacted cell.
XX Disclosure; SEQ ID NO 67; 188pp; English.
XX The invention relates to a method of determining (M1) clostridial toxin
XX activity, comprising contacting cell with sample comprising clostridial
XX toxin substrate with donor fluorophore (F), acceptor (A) with an
XX absorbance spectrum overlapping emission spectrum of fluorophore
XX between (F) and (A), where under appropriate conditions resonance
XX transfer is exhibited between fluorophore and acceptor, exciting the
XX donor fluorophore, and determining resonance energy transfer of the
XX contacted cell relative to a control cell, where a difference in
XX resonance energy transfer of the contacted cell as compared to the
XX control cell is indicative of clostridial toxin activity. (M1) is useful
XX for determining clostridial toxin activity, where the sample is a crude
XX cell lysate, isolated clostridial toxin, formulated clostridial toxin
XX product, BOTOX or food. (M1) is an automated high-throughput assay. (M1)
XX reduces the need for animal toxicity studies and serves to analyze
XX multiple toxin functions such as binding a cellular uptake of the toxin,
XX translocation into the cell cytosol and protease activity. In the method
XX M1, the clostridial toxin substrate is a botulinum toxin substrate
XX selected from a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G
XX or TeNT substrate comprising a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E,
XX BONT/F, BONT/G or TeNT recognition sequence. This sequence corresponds to
XX a recognition sequence for a botulinum toxin used as the clostridial
XX toxin substrate.
XX Sequence 16 AA;
XX Query Match 100.0%; Score 79; DB 8; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 4.5e-07;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SNKTRIDEANQRATKM 16
Db |||||
1 SNKTRIDEANQRATKM 16
RESULT 6
AEA14919
ID AEA14919 standard; peptide; 16 AA.
XX AEA14919;
XX 14-JUL-2005 (first entry)
XX Human SNAP-25 substrate BONT/A recognition sequence, SEQ ID NO: 29.
XX Neurotoxin; fluorescence; SNAP-25; botulinum toxin.
XX Homo sapiens.
XX US2005100973-A1.
XX

PD 12-MAY-2005.
 XX
 PF 13-AUG-2004; 2004US-00917844.
 XX
 PR 28-AUG-2001; 2001US-00942098.
 XX
 PA (ALLR) ALLERGAN SALES INC.
 XX
 PI Steward LE, Gilmore MA, Aoki KR;
 XX
 DR WPI; 2005-365632/37.
 XX
 XX Determining clostridial toxin protease activity, by treating sample with
 PT tagged toxin substrate comprising fluorescent protein, first and second
 PT partner of affinity couple and assaying fluorescent cleavage product in
 PT treated sample.
 XX
 XX Disclosure; SEQ ID NO 29; 97pp; English.
 PS
 XX The present invention relates to a method for determining protease
 CC activity of clostridial neurotoxins such as botulinum neurotoxin (BoNT)
 CC and tetanus neurotoxin (TeNT). The method involves treating with a
 CC sample, in solution phase under conditions suitable for clostridial toxin
 CC protease activity, a tagged toxin substrate (e.g. SNAP-25, VAMP,
 CC syntaxin) comprising fluorescent protein, first partner of affinity
 CC couple and clostridial toxin recognition sequence comprising cleavage
 CC site; contacting treated sample with second partner of affinity couple;
 CC and assaying presence of fluorescent cleavage product in the treated
 CC sample. The present sequence is the human SNAP-25 substrate BoNT/A
 CC (botulinum neurotoxin serotype A) recognition sequence.
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 79; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SNKTRIDEANQRATKM 16
 Db |||||
 1 SNKTRIDEANQRATKM 16
 RESULT 7
 AAY44057
 ID AAY44057 standard; peptide; 17 AA.
 XX
 AC AAY44057;
 XX
 DT 18-JAN-2000 (first entry)
 XX
 DE Human SNAP25 (amino acids 187-203) analogue #36.
 XX
 KW Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;
 KW fluorescamine; detection; human; synaptosomal protein; SNAP25;
 KW hydrolysis; amino group.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US9565699-A.
 XX
 DT 12-OCT-1999.
 XX
 DE Quantitation of type A botulinum toxin.
 XX
 PF Claim 1; Col 4; 28pp; English.
 XX
 PS The invention relates to an enzymatic assay for the quantitation of type
 CC A botulinum toxin, by determining the proteolytic activity of botulinum
 CC neurotoxin type A using fluorescamine detection. The method comprises
 CC adding an analogue (e.g. AAY44022-Y44076) of this peptide (which
 CC represents amino acids 187-203 of the human synaptosomal protein SNAP25)
 CC to a sample containing the botulinum toxin A so that hydrolysis of the
 CC peptide is initiated, then stopping hydrolysis of the peptide at
 CC different time points; and measuring the amount of hydrolysis at each

PT Quantitation of type A botulinum toxin.
 XX
 PS Disclosure; Col 9; 28pp; English.
 XX
 CC The invention relates to an enzymatic assay for the quantitation of type
 CC A botulinum toxin, by determining the proteolytic activity of botulinum
 CC neurotoxin type A using fluorescamine detection. Botulinum toxin A has
 CC been shown to cleave the synaptosomal neurotransmitter peptide SNAP25
 CC between residues 197-198. The method comprises adding an analogue (e.g.
 CC AAY44022-Y44076) of the SNAP25 peptide (AAY44021, amino acids 187-203 of
 CC human SNAP25) to a sample containing the botulinum toxin A so that
 CC hydrolysis of the peptide is initiated, then stopping hydrolysis of the
 CC peptide at different time points; and measuring the amount of hydrolysis
 CC at each time point by combining with a label capable of detecting free
 CC amino groups resulting from the hydrolysis. The amount of botulinum toxin
 CC A present in the sample is determined by comparing measurements with the
 CC amount of label produced from a known concentration of toxin measured
 CC under similar conditions. The method is useful for the quantitation of
 CC type A botulinum toxin
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 79; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SNKTRIDEANQRATKM 16
 Db |||||
 1 SNKTRIDEANQRATKM 16
 RESULT 8
 AAY44021
 ID AAY44021 standard; peptide; 17 AA.
 XX
 AC AAY44021;
 XX
 DT 18-JAN-2000 (first entry)
 XX
 DE Amino acids 187-203 of human SNAP25.
 XX
 KW Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;
 KW fluorescamine; detection; human; synaptosomal protein; SNAP25;
 KW hydrolysis; amino group.
 XX
 OS Homo sapiens.
 XX
 PN US9565699-A.
 XX
 DT 12-OCT-1999.
 XX
 DE Quantitation of type A botulinum toxin.
 XX
 PF Claim 1; Col 4; 28pp; English.
 XX
 PS The invention relates to an enzymatic assay for the quantitation of type
 CC A botulinum toxin, by determining the proteolytic activity of botulinum
 CC neurotoxin type A using fluorescamine detection. The method comprises
 CC adding an analogue (e.g. AAY44022-Y44076) of this peptide (which
 CC represents amino acids 187-203 of the human synaptosomal protein SNAP25)
 CC to a sample containing the botulinum toxin A so that hydrolysis of the
 CC peptide is initiated, then stopping hydrolysis of the peptide at
 CC different time points; and measuring the amount of hydrolysis at each

CC time point by combining with a label capable of detecting free amino
 CC groups resulting from the hydrolysis. The amount of botulinum toxin A
 CC present in the sample is determined by comparing measurements with the
 CC amount of label produced from a known concentration of toxin measured
 CC under similar conditions. The method is useful for the quantitation of
 CC type A botulinum toxin

XX SQ Sequence 17 AA;
 Query Match 100.0%; Score 79; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKM 16
 |||||
 DB 1 SNKTRIDEANQRATKM 16

RESULT 9
 ABG69065
 ID ABG69065 standard; peptide; 17 AA.
 AC
 AC ABG69065;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Human polypeptide C-terminal fragment.
 XX
 KW Botulinum neurotoxin light chain; BoNT LC; botulism; dystonia; pain;
 KW spasticity; ocular motility; facial dyskinesia; stiff-person syndrome;
 KW bladder dysfunction; segmental myoclonus; hyperkinetic disorder; human;
 KW cosmetic treatment; facial wrinkle; cerebellar palsy; analgesic; relaxant;
 KW lower motor neuron hyperactivity; autonomic nerve function; muscular;
 KW immunostimulant; antibacterial.
 XX
 OS Homo sapiens.
 XX
 FN WO200236758-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 06-NOV-2001; 2001WO-US047230.
 XX
 XX 06-NOV-2000; 2000US-0246774P.
 PR 20-JUL-2001; 2001US-00910186.
 PR 09-AUG-2001; 2001US-0311966P.
 XX
 PA (USSA) US ARMY MEDICAL RES & MATERIAL COMMAND.
 XX
 PI Smith LA, Jensen M;
 XX
 DR WPI; 2002-575192/61.
 XX
 PT Novel nucleic acid molecule encoding botulinum neurotoxin light chain
 PT serotype A, useful for producing the neurotoxin for vaccination against
 PT botulism, comprises sequence expressible in host other than Clostridium.
 XX
 PS Example 25; Page 62; 166pp; English.
 XX
 CC The invention relates to a nucleic acid molecule encoding a botulinum
 CC neurotoxin light chain (BoNT LC) serotype A, where the DNA has a sequence
 CC that is expressible in a host organism other than Clostridium, or has a
 CC total A+T content that is less than about 70%. The BoNT LC protein is
 CC useful in vaccination against botulism, for eliciting protective immunity
 CC in a mammal, for treating dystonias, spasticity, pain, ocular motility,
 CC facial dyskinesias, stiff-person syndrome, bladder dysfunction, segmental
 CC myoclonus, hyperkinetic disorders, cosmetic treatment of facial wrinkles,
 CC conditions characterised by hyperactivity of the lower motor neuron, and
 CC to control autonomic nerve function or tiptoe-walking due to stiff
 CC muscles common in children with cerebral palsy. The sequences are also
 CC useful for screening for botulinum neurotoxin inhibitors. This sequence
 CC represents a human polypeptide C-terminal fragment, used in the scope of
 CC the invention

XX SQ Sequence 17 AA;
 Query Match 100.0%; Score 79; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKM 16
 |||||
 DB 1 SNKTRIDEANQRATKM 16

RESULT 10
 AAE36675
 ID AAE36675 standard; peptide; 17 AA.
 XX
 AC AAE36675;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE Human SNAP-25 peptide #6.
 XX
 KW Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW cosmetic.
 XX
 OS Homo sapiens.
 XX
 FN WO2003020948-A2.
 XX
 PD 13-MAR-2003.
 XX
 PF 22-AUG-2002; 2002WO-US027145.
 XX
 PR 28-AUG-2001; 2001US-00942024.
 XX
 PA (ALLR) ALLERGAN INC.
 XX
 PI Steward LE, Fernandez-Salas E, Aoki KR;
 XX
 DR WPI; 2003-290198/28.
 XX
 PT Botulinum serotype A/E substrate useful for assaying protease activity of
 PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 PT toxin recognition sequence that includes a cleavage site.
 XX
 PS Disclosure; Page 40; 168pp; English.
 XX
 CC The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is human
 CC SNAP-25 peptide used in the invention

XX SQ Sequence 17 AA;
 Query Match 100.0%; Score 79; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;

```
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKM 16
DB 1 SNKTRIDEANORATKM 16
|||||

RESULT 11
AAE36676
ID AAE36676 standard; peptide; 17 AA.
AC AAE36676;
XX
DT 07-AUG-2003 (first entry)
XX
DE Human SNAP-25 peptide #7.
XX
KW Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
KW cosmetic.
XX
OS Homo sapiens.
XX
PN WO2003020948-A2.
XX
PD 13-MAR-2003.
XX
PF 22-AUG-2002; 2002WO-US027145.
XX
PR 28-AUG-2001; 2001US-00942024.
XX
PA (ALLR ) ALLERGAN INC.
XX
PI Steward LE, Fernandez-Salas E, Aoki KR;
XX WPI; 2003-290198/28.
XX
PT Botulinum serotype A/E substrate useful for assaying protease activity of
PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
PT toxin recognition sequence that includes a cleavage site.
XX
PS Disclosure; Page 40; 168pp; English.
XX
CC The present invention relates to novel clostridium toxin substrates. The
CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
CC which comprise a donor fluorophore, an acceptor having an absorbance and a
CC spectrum overlapping the emission spectrum of the donor fluorophore and a
CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
CC the cleavage site intervenes between the donor fluorophore and acceptor
CC and under the appropriate conditions, the resonance energy transfer is
CC exhibited between the donor and acceptor. Natural targets of clostridium
CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
CC of the invention are useful in assaying for the protease activity of any
CC clostridial toxin including botulinum toxins of all serotypes and tetanus
CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
CC samples, water samples, cosmetics, tissue samples and beverage or food
CC samples. They are useful to assay a sample from a human or animal, for
CC e.g., exposed to clostridial toxin or having one or more symptoms of a
CC clostridial toxin, to follow activity during production and purification
CC of clostridial toxin and to assay formulated clostridial toxin products
CC including pharmaceuticals and cosmetics. The present sequence is human
CC SNAP-25 peptide used in the invention
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 79; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKM 16
DB 2 SNKTRIDEANORATKM 17
|||||

RESULT 12
ABW01732
ID ABW01732 standard; peptide; 17 AA.
XX
AC ABW01732;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human SNAP-25 BoNT/A recognition peptide #5.
XX
KW Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
KW human.
XX
OS Homo sapiens.
XX
PN US2003143651-A1.
XX
PD 31-JUL-2003.
XX
PF 28-AUG-2001; 2001US-00942098.
XX
PR 28-AUG-2001; 2001US-00942098.
XX
PA (STEW/) STEWARD L E.
PA (FERN/) FERNANDEZ-SALAS E.
PA (AOKI/) AOKI K R.
XX
PI Steward LE, Fernandez-Salas E, Aoki KR;
XX WPI; 2003-829791/77.
XX
PT Determining clostridial toxin protease activity, by treating sample with
PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
PT sequence, under conditions which exhibit resonance energy transfer.
XX
PS Disclosure; Page 10; 0pp; English.
XX
CC The present invention provides clostridial toxin substrates useful in
CC assaying for the protease activity of any clostridial toxin including
CC toxins of all serotypes as well as tetanus toxins. The present sequence
CC is human SNAP-25 BoNT/A (botulinum neurotoxin serotype A) recognition
CC peptide
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 79; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKM 16
DB 2 SNKTRIDEANORATKM 17
|||||

RESULT 13
ABW01731
ID ABW01731 standard; peptide; 17 AA.
XX
AC ABW01731;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human SNAP-25 BoNT/A recognition peptide #4.
XX
KW Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
KW human.
XX
OS Homo sapiens.
XX
PN US2003143651-A1.
XX
```

PD 31-JUL-2003.
 XX
 XX 28-AUG-2001; 2001US-00942098.
 PP
 XX 28-AUG-2001; 2001US-00942098.
 PR
 XX (STEW/) STEWARD L E.
 PA (PERN/) FERNANDEZ-SALAS E.
 PA (AOKI/) AOKI K R.
 XX
 XX Steward LE, Fernandez-Salas E, Aoki KR;
 PI
 XX WPI; 2003-829791/77.
 DR
 XX Determining clostridial toxin protease activity, by treating sample with
 XX clostridial substrate with donor fluorophore, acceptor, toxin recognition
 PT sequence, under conditions which exhibit resonance energy transfer.
 PT
 XX Disclosure; Page 10; opp; English.
 PS
 XX The present invention provides clostridial toxin substrates useful in
 CC assaying for the protease activity of any clostridial toxin including
 CC toxins of all serotypes as well as tetanus toxins. The present sequence
 CC is human SNAP-25 BONT/A (botulinum neurotoxin serotype A) recognition
 CC peptide
 CC
 XX Sequence 17 AA;
 SQ
 Query Match 100.0%; Score 79; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNKTRIDEANORATKM 16
 DB |||||
 1 SNKTRIDEANORATKM 16
 RESULT 14
 ADM97046
 ID ADM97046 standard; peptide; 17 AA.
 XX
 AC ADM97046;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Botulinum toxin substrate recognition sequence #31.
 XX
 KW clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.
 XX
 OS Homo sapiens.
 XX
 FN WO2004029576-A2.
 XX
 PD 08-APR-2004.
 XX
 PF 04-SEP-2003; 2003WO-US028092.
 XX
 PR 27-SEP-2002; 2002US-00261161.
 XX
 PA (ALLR) ALLERGAN INC.
 XX
 PI Fernandez-Salas E, Steward LE, Aoki KR;
 XX
 XX WPI; 2004-340456/31.
 DR
 XX Determining clostridial toxin activity, comprises contacting cell with
 PT sample comprising substrate with donor fluorophore, acceptor and
 PT recognition sequence, exciting fluorophore, and determining resonance
 PT energy transfer of contacted cell.
 XX
 PS Disclosure; SEQ ID NO 52; 188pp; English.
 XX
 XX The invention relates to a method of determining (M1) clostridial toxin

CC activity, comprising contacting cell with sample comprising clostridial
 CC toxin substrate with donor fluorophore (F), acceptor (A) with an
 CC absorbance spectrum overlapping emission spectrum of fluorophore
 CC clostridial toxin recognition sequence with cleavage site intervening
 CC between (F) and (A), where under appropriate conditions resonance
 CC transfer is exhibited between fluorophore and acceptor, exciting the
 CC donor fluorophore, and determining resonance energy transfer of the
 CC contacted cell relative to a control cell, where a difference in
 CC resonance energy transfer of the contacted cell as compared to the
 CC control cell is indicative of clostridial toxin activity. (M1) is useful
 CC for determining clostridial toxin activity, where the sample is a crude
 CC cell lysate, isolated clostridial toxin, formulated clostridial toxin
 CC product, BOTOX or food. (M1) is an automated high-throughput assay. (M1)
 CC reduces the need for animal toxicity studies and serves to analyze
 CC multiple toxin functions such as binding a cellular uptake of the toxin,
 CC translocation into the cell cytosol and protease activity. In the method
 CC M1, the clostridial toxin substrate is a botulinum toxin substrate
 CC selected from a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G
 CC or TeNT substrate comprising a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G,
 CC BONT/F, BONT/G or TeNT recognition sequence. This sequence corresponds to
 CC a recognition sequence for a botulinum toxin used as the clostridial
 CC toxin substrate.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 79; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNKTRIDEANORATKM 16
 DB |||||
 1 SNKTRIDEANORATKM 16
 RESULT 15
 ADM97062
 ID ADM97062 standard; peptide; 17 AA.
 XX
 AC ADM97062;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Botulinum toxin substrate recognition sequence #47.
 XX
 KW clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.
 XX
 OS Synthetic.
 XX
 FN WO2004029576-A2.
 XX
 PD 08-APR-2004.
 XX
 PF 04-SEP-2003; 2003WO-US028092.
 XX
 PR 27-SEP-2002; 2002US-00261161.
 XX
 PA (ALLR) ALLERGAN INC.
 XX
 PI Fernandez-Salas E, Steward LE, Aoki KR;
 XX
 XX WPI; 2004-340456/31.
 DR
 XX Determining clostridial toxin activity, comprises contacting cell with
 PT sample comprising substrate with donor fluorophore, acceptor and
 PT recognition sequence, exciting fluorophore, and determining resonance
 PT energy transfer of contacted cell.
 XX
 PS Disclosure; SEQ ID NO 68; 188pp; English.
 XX
 XX The invention relates to a method of determining (M1) clostridial toxin

CC activity, comprising contacting cell with sample comprising clostridial
 CC toxin substrate with donor fluorophore (F), acceptor (A) with an
 CC absorbance spectrum overlapping emission spectrum of fluorophore
 CC clostridial toxin recognition sequence with cleavage site intervening
 CC between (F) and (A), where under appropriate conditions resonance
 CC transfer is exhibited between fluorophore and acceptor, exciting the
 CC donor fluorophore, and determining resonance energy transfer of the
 CC contacted cell relative to a control cell, where a difference in
 CC resonance energy transfer of the contacted cell as compared to the
 CC control cell is indicative of clostridial toxin activity. (M1) is useful
 CC for determining clostridial toxin activity, where the sample is a crude
 CC cell lysate, isolated clostridial toxin, formulated clostridial toxin
 CC product, BOTOX or food. (M1) is an automated high-throughput assay. (M1)
 CC reduces the need for animal toxicity studies and serves to analyze
 CC multiple toxin functions such as binding a cellular uptake of the toxin,
 CC translocation into the cell cytosol and protease activity. In the method
 CC M1, the clostridial toxin substrate is a botulinum toxin substrate
 CC selected from a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G
 CC or TeNT substrate comprising a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G,
 CC BONT/F, BONT/G or TeNT recognition sequence. This sequence corresponds to
 CC a recognition sequence for a botulinum toxin used as the clostridial
 CC toxin substrate.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 79; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNKTRIDEANORATKM 16
 DB |||||
 1 SNKTRIDEANORATKM 16
 RESULT 15
 ADM97062
 ID ADM97062 standard; peptide; 17 AA.
 XX
 AC ADM97062;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Botulinum toxin substrate recognition sequence #47.
 XX
 KW clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.
 XX
 OS Synthetic.
 XX
 FN WO2004029576-A2.
 XX
 PD 08-APR-2004.
 XX
 PF 04-SEP-2003; 2003WO-US028092.
 XX
 PR 27-SEP-2002; 2002US-00261161.
 XX
 PA (ALLR) ALLERGAN INC.
 XX
 PI Fernandez-Salas E, Steward LE, Aoki KR;
 XX
 XX WPI; 2004-340456/31.
 DR
 XX Determining clostridial toxin activity, comprises contacting cell with
 PT sample comprising substrate with donor fluorophore, acceptor and
 PT recognition sequence, exciting fluorophore, and determining resonance
 PT energy transfer of contacted cell.
 XX
 PS Disclosure; SEQ ID NO 68; 188pp; English.
 XX
 XX The invention relates to a method of determining (M1) clostridial toxin

CC clostridial toxin recognition sequence with cleavage site intervening
 CC between (F) and (A), where under appropriate conditions resonance
 CC transfer is exhibited between fluorophore and acceptor, exciting the
 CC donor fluorophore, and determining resonance energy transfer of the
 CC contacted cell relative to a control cell, where a difference in
 CC resonance energy transfer of the contacted cell as compared to the
 CC control cell is indicative of clostridial toxin activity. (M1) is useful
 CC for determining clostridial toxin activity, where the sample is a crude
 CC cell lysate, isolated clostridial toxin, formulated clostridial toxin
 CC product, BOTOX or food. (M1) is an automated high-throughput assay.
 CC reduces the need for animal toxicity studies and serves to analyze
 CC multiple toxin functions such as binding a cellular uptake of the toxin,
 CC translocation into the cell cytosol and protease activity. In the method
 CC M1, the clostridial toxin substrate is a botulinum toxin substrate
 CC selected from a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G
 CC or TeNT substrate comprising a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E,
 CC BONT/F, BONT/G or TeNT recognition sequence. This sequence corresponds to
 CC a recognition sequence for a botulinum toxin used as the clostridial
 CC toxin substrate.

XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 79; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKM 16
 |||||
 Db 1 SNKTRIDEANQRATKM 16

Search completed: April 3, 2006, 15:36:56
 Job time : 82.2217 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:23:07 ; Search time 2.19355 Seconds
(without alignments)

235.925 Million cell updates/sec

Title: US-09-942-098-30

Perfect score: 83

Sequence: 1 SNKTRIDEANQRATKML 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /SIDSS5/ptodata/1/pubpaa/US08 NEW PUB.pap.*
2: /SIDSS5/ptodata/1/pubpaa/US06 NEW PUB.pap.*
3: /SIDSS5/ptodata/1/pubpaa/US07 NEW PUB.pap.*
4: /SIDSS5/ptodata/1/pubpaa/PCT_NEW PUB.pap.*
5: /SIDSS5/ptodata/1/pubpaa/US09 NEW PUB.pap.*
6: /SIDSS5/ptodata/1/pubpaa/US10 NEW PUB.pap.*
7: /SIDSS5/ptodata/1/pubpaa/US11 NEW PUB.pap.*
8: /SIDSS5/ptodata/1/pubpaa/US60 NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	83	100.0	17	6 US-10-980-346B-6
2	83	100.0	17	6 US-10-980-346B-37
3	83	100.0	17	6 US-10-947-071-33
4	83	100.0	17	6 US-10-948-097-33
5	83	100.0	18	6 US-10-947-071-35
6	83	100.0	18	6 US-10-948-097-35
7	83	100.0	33	6 US-10-947-071-36
8	83	100.0	33	6 US-10-947-071-40
9	83	100.0	33	6 US-10-947-071-41
10	83	100.0	33	6 US-10-948-097-36
11	83	100.0	33	6 US-10-948-097-40
12	83	100.0	33	6 US-10-948-097-41
13	83	100.0	116	7 US-11-195-098-11
14	83	100.0	203	6 US-10-947-071-4
15	83	100.0	203	6 US-10-948-097-4
16	83	100.0	206	6 US-10-947-071-1
17	83	100.0	206	6 US-10-947-071-2
18	83	100.0	206	6 US-10-948-097-1
19	83	100.0	206	6 US-10-948-097-2
20	83	100.0	206	7 US-11-169-041-225
21	83	100.0	334	6 US-10-947-071-20
22	83	100.0	334	6 US-10-948-097-20
23	80	96.4	17	6 US-10-947-071-61
24	80	95.4	17	6 US-10-948-097-61
25	79	95.2	16	6 US-10-947-071-32

26 79 95.2 16 6 US-10-948-097-32 Sequence 32, Appl
27 79 95.2 17 6 US-10-947-071-34 Sequence 34, Appl
28 79 95.2 17 6 US-10-947-071-53 Sequence 53, Appl
29 79 95.2 17 6 US-10-947-071-55 Sequence 55, Appl
30 79 95.2 17 6 US-10-947-071-60 Sequence 60, Appl
31 79 95.2 17 6 US-10-948-097-34 Sequence 34, Appl
32 79 95.2 17 6 US-10-948-097-53 Sequence 53, Appl
33 79 95.2 17 6 US-10-948-097-55 Sequence 55, Appl
34 79 95.2 17 6 US-10-948-097-60 Sequence 60, Appl
35 78 94.0 17 6 US-10-947-071-54 Sequence 54, Appl
36 78 94.0 17 6 US-10-947-071-58 Sequence 58, Appl
37 78 94.0 17 6 US-10-947-071-62 Sequence 62, Appl
38 78 94.0 17 6 US-10-948-097-54 Sequence 54, Appl
39 78 94.0 17 6 US-10-948-097-58 Sequence 58, Appl
40 78 94.0 17 6 US-10-948-097-62 Sequence 62, Appl
41 77 92.8 17 6 US-10-980-346B-38 Sequence 38, Appl
42 77 92.8 17 6 US-10-947-071-50 Sequence 50, Appl
43 77 92.8 17 6 US-10-947-071-51 Sequence 51, Appl
44 77 92.8 17 6 US-10-947-071-52 Sequence 52, Appl
45 77 92.8 17 6 US-10-947-071-56 Sequence 56, Appl

ALIGNMENTS

RESULT 1

US-10-980-346B-6

; Sequence 6, Application US/10980346B

; Publication No. US20060024763A1

; GENERAL INFORMATION:

; APPLICANT: Los Alamos National Laboratory

; APPLICANT: Schmidt, Jurgen G., et al.

; TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation

; TITLE OF INVENTION: of Botulinum Neurotoxins

; FILE REFERENCE: S-102,313

; CURRENT APPLICATION NUMBER: US/10/980,346B

; CURRENT FILING DATE: 2004-11-03

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6

; LENGTH: 17

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum

; OTHER INFORMATION: Neurotoxin (BoNT)

US-10-980-346B-6

Query Match 100.0%; Score 83; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 8.1e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17

Db 1 SNKTRIDEANQRATKML 17

RESULT 2

US-10-980-346B-37

; Sequence 37, Application US/10980346B

; Publication No. US20060024763A1

; GENERAL INFORMATION:

; APPLICANT: Los Alamos National Laboratory

; APPLICANT: Schmidt, Jurgen G., et al.

; TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation

; TITLE OF INVENTION: of Botulinum Neurotoxins

; FILE REFERENCE: S-102,313

; CURRENT APPLICATION NUMBER: US/10/980,346B

; CURRENT FILING DATE: 2004-11-03

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 37

; LENGTH: 17

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum
; OTHER INFORMATION: Neurotoxin (BoNT)
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(17)
; OTHER INFORMATION: amide bound at one end of the peptide
US-10-980-346B-37

Query Match      100.0%; Score 83; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 1 SNKTRIDEANQRATKML 17

RESULT 3
US-10-947-071-33
; Sequence 33, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-33

Query Match      100.0%; Score 83; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 1 SNKTRIDEANQRATKML 17

RESULT 4
US-10-948-097-33
; Sequence 33, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-33

Query Match      100.0%; Score 83; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 1 SNKTRIDEANQRATKML 17

RESULT 5
US-10-947-071-35
; Sequence 35, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-35

Query Match      100.0%; Score 83; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18

RESULT 6
US-10-948-097-35
; Sequence 35, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-35

Query Match      100.0%; Score 83; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18
```

```
US-10-948-097-33

Query Match      100.0%; Score 83; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 1 SNKTRIDEANQRATKML 17

RESULT 5
US-10-947-071-35
; Sequence 35, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-35

Query Match      100.0%; Score 83; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18

RESULT 6
US-10-948-097-35
; Sequence 35, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-35

Query Match      100.0%; Score 83; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18
```

RESULT 7
US-10-947-071-36
; Sequence 36, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-947-071-36

Query Match 100.0%; Score 83; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKML 17
Db 14 SNKTRIDEANORATKML 30
|||||

RESULT 8
US-10-947-071-40
; Sequence 40, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-40

Query Match 100.0%; Score 83; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKML 17
Db 14 SNKTRIDEANORATKML 30
|||||

RESULT 9
US-10-947-071-41
; Sequence 41, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella

; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-41

Query Match 100.0%; Score 83; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKML 17
Db 14 SNKTRIDEANORATKML 30
|||||

RESULT 10
US-10-948-097-36
; Sequence 36, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-948-097-36

Query Match 100.0%; Score 83; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKML 17
Db 14 SNKTRIDEANORATKML 30
|||||

RESULT 11
US-10-948-097-40
; Sequence 40, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-40

Query Match          100.0%; Score 83; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
   |||||
Db 14 SNKTRIDEANQRATKML 30

RESULT 12
US-10-948-097-41
; Sequence 41, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-41

Query Match          100.0%; Score 83; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
   |||||
Db 14 SNKTRIDEANQRATKML 30

RESULT 13
US-11-195-098-11
; Sequence 11, Application US/11195098
; Publication No. US20050287622A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/11/195,098
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/802,574
; PRIOR FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 09/962,360
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceiny1-cysteine
US-11-195-098-11

Query Match          100.0%; Score 83; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
   |||||
Db 96 SNKTRIDEANQRATKML 112

RESULT 14
US-10-947-071-4
; Sequence 4, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-4

Query Match          100.0%; Score 83; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
   |||||
Db 184 SNKTRIDEANQRATKML 200

RESULT 15
US-10-948-097-4
; Sequence 4, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-4

Query Match          100.0%; Score 83; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
   |||||
Db 184 SNKTRIDEANQRATKML 200
```

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKML 17
Db 184 SNKTRIDEANORATKML 200

Search completed: April 3, 2006, 15:27:29
Job time : 2.19355 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:21:47 ; Search time 16.0403 Seconds
(without alignments)
442.828 Million cell updates/sec

Title: US-09-942-098-30

Perfect score: 83

Sequence: 1 SNKTRIDEANQRATKML 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_Main.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	17	3	US-09-942-024-30
2	83	100.0	17	3	US-09-942-098-30
3	83	100.0	17	4	US-10-011-588-2
4	83	100.0	17	4	US-10-261-161-52
5	83	100.0	17	4	US-10-261-161-68
6	83	100.0	17	5	US-10-917-844-30
7	83	100.0	18	3	US-09-942-024-32
8	83	100.0	18	3	US-09-942-098-32
9	83	100.0	18	4	US-10-261-161-54
10	83	100.0	18	5	US-10-917-844-32
11	83	100.0	19	4	US-10-705-857-6
12	83	100.0	21	3	US-09-942-024-89
13	83	100.0	21	3	US-09-942-098-89
14	83	100.0	23	3	US-09-942-024-88
15	83	100.0	23	3	US-09-942-098-88
16	83	100.0	24	3	US-09-942-024-90
17	83	100.0	24	3	US-09-942-098-90
18	83	100.0	33	3	US-09-942-024-33
19	83	100.0	33	3	US-09-942-024-37
20	83	100.0	33	3	US-09-942-024-38
21	83	100.0	33	3	US-09-942-098-33
22	83	100.0	33	3	US-09-942-098-37
23	83	100.0	33	3	US-09-942-098-38
24	83	100.0	33	4	US-10-261-161-55
25	83	100.0	33	4	US-10-261-161-59
26	83	100.0	33	4	US-10-261-161-60
27	83	100.0	33	5	US-10-917-844-33

28	83	100.0	33	5	US-10-917-844-37	Sequence 37, Appl
29	83	100.0	33	5	US-10-917-844-38	Sequence 38, Appl
30	83	100.0	86	4	US-10-705-857-4	Sequence 4, Appl
31	83	100.0	114	5	US-10-917-844-112	Sequence 112, App
32	83	100.0	116	3	US-09-962-360B-11	Sequence 11, Appl
33	83	100.0	116	4	US-10-802-574-11	Sequence 11, Appl
34	83	100.0	203	3	US-09-942-024-14	Sequence 14, Appl
35	83	100.0	203	3	US-09-942-098-14	Sequence 14, Appl
36	83	100.0	203	4	US-10-261-161-7	Sequence 7, Appl
37	83	100.0	203	5	US-10-917-844-14	Sequence 14, Appl
38	83	100.0	206	3	US-09-942-024-2	Sequence 2, Appl
39	83	100.0	206	3	US-09-942-024-12	Sequence 12, Appl
40	83	100.0	206	3	US-09-942-098-2	Sequence 2, Appl
41	83	100.0	206	3	US-09-942-098-7	Sequence 7, Appl
42	83	100.0	206	3	US-09-942-098-12	Sequence 12, Appl
43	83	100.0	206	4	US-10-261-161-4	Sequence 4, Appl
44	83	100.0	206	4	US-10-261-161-5	Sequence 5, Appl
45	83	100.0	206	4	US-10-261-161-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-942-024-30
; Sequence 30, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-30

Query Match 100.0%; Score 83; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	SNKTRIDEANQRATKML	17
Db	1	SNKTRIDEANQRATKML	17

RESULT 2

US-09-942-098-30
; Sequence 30, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-30

Query Match 100.0%; Score 83; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
|||||
Db 1 SNKTRIDEANQRATKML 17

RESULT 3
US-10-011-588-2
; Sequence 2, Application US/10011588
; Publication No. US20020168727A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Leonard
; APPLICANT: Jensen, Melody
; TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS AND LIGHT CHAIN FUSION PROTEINS FOR USE IN
; TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY
; FILE REFERENCE: A34796 067252.0113
; CURRENT APPLICATION NUMBER: US/10/011,588
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 09/910,186
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/611,419
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 60/246,744
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 60/311,966
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: Residues 187-203 of SNAP-25
US-10-011-588-2

Query Match 100.0%; Score 83; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
|||||
Db 1 SNKTRIDEANQRATKML 17

RESULT 4
US-10-261-161-52
; Sequence 52, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-52

Query Match 100.0%; Score 83; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
|||||
Db 1 SNKTRIDEANQRATKML 17

RESULT 5
US-10-261-161-68
; Sequence 68, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-261-161-68

Query Match 100.0%; Score 83; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
|||||
Db 1 SNKTRIDEANQRATKML 17

RESULT 6
US-10-917-844-30
; Sequence 30, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
; APPLICANT: Aoki, Kei R.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
; FILE REFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917,844
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-844-30

Query Match 100.0%; Score 83; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
|||||
Db 1 SNKTRIDEANQRATKML 17

```
RESULT 7
US-09-942-024-32
; Sequence 32, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-32
Query Match 100.0%; Score 83; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18

RESULT 8
US-09-942-098-32
; Sequence 32, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-32
Query Match 100.0%; Score 83; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18

RESULT 9
US-10-261-161-54
; Sequence 54, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-54
Query Match 100.0%; Score 83; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18

RESULT 10
US-10-917-844-32
; Sequence 32, Application US/10917844
; Publication No. US20050100973A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Gilmore, Marcella A.
; APPLICANT: Aoki, Kei R.
; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
; FILE REFERENCE: 66872-044
; CURRENT APPLICATION NUMBER: US/10/917,844
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 09/942,098
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-844-32
Query Match 100.0%; Score 83; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 2 SNKTRIDEANQRATKML 18

RESULT 11
US-10-705-857-6
; Sequence 6, Application US/10705857
; Publication No. US20040147443A1
; GENERAL INFORMATION:
; APPLICANT: RENAU, BEATRICE
; TITLE OF INVENTION: USE OF A COMBINATION OF COMPONENTS WITH AN INHIBITORY
; TITLE OF INVENTION: SYNERGISTIC EFFECT ON CALCIUM CHANNELS TO PREVENT OR
; TITLE OF INVENTION: TREAT WRINKLES AND FINE LINES
; FILE REFERENCE: 05725.1275
; CURRENT APPLICATION NUMBER: US/10/705,857
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/427,575
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: FR 0214183
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
```

```
/ OTHER INFORMATION: peptide
US-10-705-857-6

Query Match      100.0%; Score 83; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
   |||||||
Db 3 SNKTRIDEANQRATKML 19

RESULT 12
US-09-942-024-89
; Sequence 89, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 21
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-89

Query Match      100.0%; Score 83; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
   |||||||
Db 4 SNKTRIDEANQRATKML 20

RESULT 14
US-09-942-024-88
; Sequence 88, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 23
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-88

Query Match      100.0%; Score 83; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
   |||||||
Db 3 SNKTRIDEANQRATKML 19

RESULT 15
US-09-942-098-88
; Sequence 88, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

;
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 23
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-88

Query Match 100.0%; Score 83; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
| | | | | | | | | | | | | | | | | | | | |
Db 3 SNKTRIDEANQRATKML 19

Search completed: April 3, 2006, 15:26:52
Job time : 17.0403 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:16:44 ; Search time 4.52419 Seconds
(without alignments)
310.660 Million cell updates/sec

Title: US-09-942-098-30
Perfect score: 83
Sequence: 1 SNKTRIDEANORATKML 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pdp.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pdp.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pdp.*
4: /cgn2_6/ptodata/1/iaa/PCRTUS COMB.pdp.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pdp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	17	1	US-08-743-894B-1
2	83	100.0	17	1	US-08-743-894B-37
3	83	100.0	20	2	US-08-819-286-9
4	83	100.0	26	2	US-08-819-286-8
5	83	100.0	37	2	US-08-819-286-4
6	83	100.0	70	1	US-08-760-001-10
7	83	100.0	70	2	US-09-015-960-10
8	83	100.0	70	2	US-09-534-572-10
9	83	100.0	116	2	US-09-962-360B-11
10	83	100.0	206	1	US-08-393-985-18
11	83	100.0	206	2	US-08-819-286-1
12	83	100.0	206	2	US-09-949-016-6311
13	83	100.0	219	2	US-09-949-016-10671
14	80	96.4	17	1	US-08-743-894B-18
15	80	96.4	17	1	US-08-743-894B-43
16	79	95.2	16	1	US-08-743-894B-49
17	79	95.2	17	1	US-08-743-894B-27
18	79	95.2	17	1	US-08-743-894B-30
19	79	95.2	17	1	US-08-743-894B-32
20	79	95.2	17	1	US-08-743-894B-39
21	78	94.0	17	1	US-08-743-894B-19
22	78	94.0	17	1	US-08-743-894B-25
23	78	94.0	17	1	US-08-743-894B-29
24	78	94.0	17	1	US-08-743-894B-42
25	78	94.0	17	1	US-08-743-894B-50
26	77	92.8	17	1	US-08-743-894B-2
27	77	92.8	17	1	US-08-743-894B-20

28	77	92.8	17	1	US-08-743-894B-24	Sequence 24, Appl
29	77	92.8	17	1	US-08-743-894B-26	Sequence 26, Appl
30	77	92.8	17	1	US-08-743-894B-28	Sequence 28, Appl
31	77	92.8	17	1	US-08-743-894B-31	Sequence 31, Appl
32	77	92.8	17	1	US-08-743-894B-33	Sequence 33, Appl
33	77	92.8	17	1	US-08-743-894B-34	Sequence 34, Appl
34	77	92.8	17	1	US-08-743-894B-36	Sequence 36, Appl
35	77	92.8	17	1	US-08-743-894B-44	Sequence 44, Appl
36	77	92.8	17	1	US-08-743-894B-45	Sequence 45, Appl
37	77	92.8	17	1	US-08-743-894B-46	Sequence 46, Appl
38	77	92.8	24	2	US-09-962-360B-8	Sequence 8, Appl
39	77	92.8	116	2	US-09-962-360B-12	Sequence 12, Appl
40	75	90.4	17	1	US-08-743-894B-21	Sequence 21, Appl
41	75	90.4	17	1	US-08-743-894B-35	Sequence 35, Appl
42	75	90.4	17	1	US-08-743-894B-47	Sequence 47, Appl
43	75	90.4	17	1	US-08-743-894B-48	Sequence 48, Appl
44	74	89.2	15	1	US-08-743-894B-38	Sequence 38, Appl
45	74	89.2	17	1	US-08-743-894B-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-743-894B-1
; Sequence 1, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA WMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08743.894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-743-894B-1

Query Match 100.0%; Score 83; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNKTRIDEANORATKML 17
Db 1 SNKTRIDEANORATKML 17

```
RESULT 2
US-08-743-894B-37
; Sequence 37, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699member 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
US-08-743-894B-37
Query Match 100.0%; Score 83; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 1 SNKTRIDEANQRATKML 17

RESULT 3
US-08-819-286-9
; Sequence 9, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PPPTIDE INHIBITORS OF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; MEDIUM TYPE: Floppy disk
```

```
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; Molecule Type: peptide
US-08-819-286-9
Query Match 100.0%; Score 83; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANQRATKML 17
Db 1 SNKTRIDEANQRATKML 17

RESULT 4
US-08-819-286-8
; Sequence 8, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
```

TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-819-286-8
Query Match 100.0%; Score 83; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SNKTRIDEANQRATKML 17
Db 7 SNKTRIDEANQRATKML 23

RESULT 5
US-08-819-286-4
Sequence 4, Application US/08819286
Patent No. 6169074
GENERAL INFORMATION:
APPLICANT: Montcal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-819-286-4
Query Match 100.0%; Score 83; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SNKTRIDEANQRATKML 17
Db 18 SNKTRIDEANQRATKML 34

RESULT 6
US-08-760-001-10
Sequence 10, Application US/08760001
Patent No. 5962637
GENERAL INFORMATION:

APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,001
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-760-001-10
Query Match 100.0%; Score 83; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SNKTRIDEANQRATKML 17
Db 51 SNKTRIDEANQRATKML 67
RESULT 7
US-09-015-960-10
Sequence 10, Application US/09015960
Patent No. 6043042
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,960
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-015-960-10

Query Match 100.0%; Score 83; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
Db 51 SNKTRIDEANQRATKML 67

RESULT 8
US-09-534-572-10
; Sequence 10, Application US/09534572
; Patent No. 6337386
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam A. F.
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,572
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,960
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE: 30-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120003
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-534-572-10

Query Match 100.0%; Score 83; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
Db 51 SNKTRIDEANQRATKML 67

RESULT 9
US-09-962-360B-11
; Sequence 11, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; FILE REFERENCE: Neurotoxins
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoreseceinyl-cysteine
; US-09-962-360B-11

Query Match 100.0%; Score 83; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17
Db 96 SNKTRIDEANQRATKML 112

RESULT 10
US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Scheller, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA


```
Query Match          100.0%; Score 83; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 9.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SNKTRIDEANQRATKML 17
      |||||
Db      200 SNKTRIDEANQRATKML 216

RESULT 14
US-08-743-894B-18
; Sequence 18, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
US-08-743-894B-18

Query Match          96.4%; Score 80; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.7e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SNKTRIDEANQRATKML 17
      |||||
Db      1 SNKTRIDEANQRATKML 17

RESULT 15
US-08-743-894B-43
; Sequence 43, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
```

```
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
US-08-743-894B-43

Query Match          96.4%; Score 80; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.7e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SNKTRIDEANQRATKML 17
      |||||
Db      1 SNKTRIDEANQRATKML 17

Search completed: April 3, 2006, 15:17:59
Job time : 4.52419 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:49:32 ; Search time 12.7706 Seconds
(without alignments)
57.210 Million cell updates/sec

Title: US-09-942-098-90

Perfect score: 109

Sequence: 1 XADSNKTRIDEANQRATKMLGSGX 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 40 summaries

Database : Published Applications AA New:
1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pep.*
2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep.*
3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep.*
4: /SIDSS/ptodata/1/pubpaa/ECT_NEW PUB.pep.*
5: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pep.*
6: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep.*
7: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep.*
8: /SIDSS/ptodata/1/pubpaa/US60_NEW PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	100.0	33	6 US-10-947-071-36	Sequence 36, Appl
2	109	100.0	33	6 US-10-947-071-40	Sequence 40, Appl
3	109	100.0	33	6 US-10-947-071-41	Sequence 41, Appl
4	109	100.0	33	6 US-10-948-097-36	Sequence 36, Appl
5	109	100.0	33	6 US-10-948-097-40	Sequence 40, Appl
6	109	100.0	33	6 US-10-948-097-41	Sequence 41, Appl
7	109	100.0	116	7 US-11-195-098-11	Sequence 11, Appl
8	109	100.0	203	6 US-10-947-071-4	Sequence 4, Appl
9	109	100.0	203	6 US-10-948-097-4	Sequence 4, Appl
10	109	100.0	206	6 US-10-947-071-1	Sequence 1, Appl
11	109	100.0	206	6 US-10-947-071-2	Sequence 2, Appl
12	109	100.0	206	6 US-10-948-097-1	Sequence 1, Appl
13	109	100.0	206	6 US-10-948-097-2	Sequence 2, Appl
14	109	100.0	206	7 US-11-169-041-225	Sequence 225, App
15	109	100.0	334	6 US-10-947-071-20	Sequence 20, Appl
16	109	100.0	334	6 US-10-948-097-20	Sequence 20, Appl
17	109	94.5	116	7 US-11-195-098-12	Sequence 12, Appl
18	89	81.7	18	6 US-10-947-071-35	Sequence 35, Appl
19	89	81.7	18	6 US-10-948-097-35	Sequence 35, Appl
20	89	81.7	24	7 US-11-195-098-8	Sequence 8, Appl
21	85	78.0	17	6 US-10-947-071-34	Sequence 34, Appl
22	85	78.0	17	6 US-10-948-097-34	Sequence 34, Appl
23	83	76.1	17	6 US-10-980-346B-6	Sequence 6, Appl
24	83	76.1	17	6 US-10-980-346B-37	Sequence 37, Appl
25	83	76.1	17	6 US-10-947-071-33	Sequence 33, Appl

26	83	76.1	17	6 US-10-948-097-33	Sequence 33, Appl
27	83	76.1	22	6 US-10-980-346B-1	Sequence 1, Appl
28	80	73.4	17	6 US-10-947-071-61	Sequence 61, Appl
29	80	73.4	17	6 US-10-948-097-61	Sequence 61, Appl
30	79	72.5	16	6 US-10-947-071-32	Sequence 32, Appl
31	79	72.5	16	6 US-10-948-097-32	Sequence 32, Appl
32	79	72.5	17	6 US-10-947-071-53	Sequence 53, Appl
33	79	72.5	17	6 US-10-947-071-55	Sequence 55, Appl
34	79	72.5	17	6 US-10-947-071-60	Sequence 60, Appl
35	79	72.5	17	6 US-10-948-097-53	Sequence 53, Appl
36	79	72.5	17	6 US-10-948-097-55	Sequence 55, Appl
37	79	72.5	17	6 US-10-948-097-60	Sequence 60, Appl
38	78	71.6	17	6 US-10-947-071-54	Sequence 54, Appl
39	78	71.6	17	6 US-10-947-071-58	Sequence 58, Appl
40	78	71.6	17	6 US-10-947-071-62	Sequence 62, Appl
41	78	71.6	17	6 US-10-948-097-54	Sequence 54, Appl
42	78	71.6	17	6 US-10-948-097-58	Sequence 58, Appl
43	78	71.6	17	6 US-10-948-097-62	Sequence 62, Appl
44	77	70.6	17	6 US-10-980-346B-38	Sequence 38, Appl
45	77	70.6	17	6 US-10-947-071-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-10-947-071-36
; Sequence 36, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947.071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-947-071-36
Query Match 100.0%; Score 109; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.8e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ADSNKTTRIDEANQRATKMLGSG 23
DB 12 ADSNKTTRIDEANQRATKMLGSG 33
RESULT 2
US-10-947-071-40
; Sequence 40, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947.071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-40

Query Match          100.0%; Score 109; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.8e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTIDEANQRATKMLGSG 23
Db 12 ADSNKTIDEANQRATKMLGSG 33

RESULT 3
US-10-947-071-41
; Sequence 41, Application US/10947071
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-41

Query Match          100.0%; Score 109; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.8e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTIDEANQRATKMLGSG 23
Db 12 ADSNKTIDEANQRATKMLGSG 33

RESULT 4
US-10-948-097-36
; Sequence 36, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-948-097-36

Query Match          100.0%; Score 109; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.8e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTIDEANQRATKMLGSG 23
Db 12 ADSNKTIDEANQRATKMLGSG 33

RESULT 5
US-10-948-097-40
; Sequence 40, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-40

Query Match          100.0%; Score 109; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.8e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTIDEANQRATKMLGSG 23
Db 12 ADSNKTIDEANQRATKMLGSG 33

RESULT 6
US-10-948-097-41
; Sequence 41, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-41

Query Match          100.0%; Score 109; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.8e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTIDEANQRATKMLGSG 23
Db 12 ADSNKTIDEANQRATKMLGSG 33

RESULT 7
US-11-195-098-11
```

```
; Sequence 11, Application US/11195098
; Publication No. US20050287622A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/11/195,098
; PRIOR FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/802,574
; PRIOR FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 09/962,360
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-11-195-098-11

Query Match      100.0%; Score 109; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ADSNKTTRIDEANQRATKMLGSG 23
Db      94 ADSNKTTRIDEANQRATKMLGSG 115

RESULT 8
US-10-947-071-4
; Sequence 4, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-4

Query Match      100.0%; Score 109; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 5.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ADSNKTTRIDEANQRATKMLGSG 23
Db      182 ADSNKTTRIDEANQRATKMLGSG 203

RESULT 9
US-10-948-097-4

Query Match      100.0%; Score 109; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 5.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ADSNKTTRIDEANQRATKMLGSG 23
Db      182 ADSNKTTRIDEANQRATKMLGSG 203

RESULT 10
US-10-947-071-1
; Sequence 1, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-1

Query Match      100.0%; Score 109; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ADSNKTTRIDEANQRATKMLGSG 23
Db      185 ADSNKTTRIDEANQRATKMLGSG 206

RESULT 11
US-10-947-071-2
; Sequence 2, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
```

```
; Sequence 4, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-4

Query Match      100.0%; Score 109; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 5.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ADSNKTTRIDEANQRATKMLGSG 23
Db      182 ADSNKTTRIDEANQRATKMLGSG 203

RESULT 10
US-10-947-071-1
; Sequence 1, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-1

Query Match      100.0%; Score 109; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ADSNKTTRIDEANQRATKMLGSG 23
Db      185 ADSNKTTRIDEANQRATKMLGSG 206

RESULT 11
US-10-947-071-2
; Sequence 2, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
```

```
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-947-071-2

Query Match      100.0%; Score 109; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTTRIDEANORATKMLGSG 23
Db 185 ADSNKTTRIDEANORATKMLGSG 206

RESULT 12
US-10-948-097-1
; Sequence 1, Application US/10948097
; Publication No. US2006063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-1

Query Match      100.0%; Score 109; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTTRIDEANORATKMLGSG 23
Db 185 ADSNKTTRIDEANORATKMLGSG 206

RESULT 13
US-10-948-097-2
; Sequence 2, Application US/10948097
; Publication No. US2006063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
```

```
; ORGANISM: Mus musculus
US-10-948-097-2

Query Match      100.0%; Score 109; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTTRIDEANORATKMLGSG 23
Db 185 ADSNKTTRIDEANORATKMLGSG 206

RESULT 14
US-11-169-041-225
; Sequence 225, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 225
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-225

Query Match      100.0%; Score 109; DB 7; Length 206;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTTRIDEANORATKMLGSG 23
Db 185 ADSNKTTRIDEANORATKMLGSG 206

RESULT 15
US-10-947-071-20
; Sequence 20, Application US/10947071
; Publication No. US2006063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pGBI GFP-SNAP25
US-10-947-071-20

Query Match      100.0%; Score 109; DB 6; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


THIS PAGE BLANK (USPTO)

1	109	100.0	24	3	US-09-942-024-90	Sequence 90, Appl
2	109	100.0	24	3	US-09-942-028-90	Sequence 90, Appl
3	109	100.0	23	3	US-09-942-024-33	Sequence 33, Appl
4	109	100.0	33	3	US-09-942-024-37	Sequence 37, Appl
5	109	100.0	33	3	US-09-942-024-38	Sequence 38, Appl
6	109	100.0	33	3	US-09-942-024-38	Sequence 33, Appl
7	109	100.0	33	3	US-09-942-024-38	Sequence 37, Appl
8	109	100.0	33	3	US-09-942-028-37	Sequence 38, Appl
9	109	100.0	33	4	US-09-942-028-38	Sequence 55, Appl
10	109	100.0	33	4	US-10-261-161-55	Sequence 55, Appl
11	109	100.0	33	4	US-10-261-161-59	Sequence 59, Appl
12	109	100.0	33	4	US-10-261-161-60	Sequence 60, Appl
13	109	100.0	33	5	US-10-917-844-33	Sequence 33, Appl
14	109	100.0	33	5	US-10-917-844-37	Sequence 37, Appl
15	109	100.0	33	5	US-10-917-844-38	Sequence 38, Appl
16	109	100.0	86	4	US-10-705-857-4	Sequence 4, Appl
17	109	100.0	114	5	US-10-917-844-112	Sequence 112, Appl
18	109	100.0	116	3	US-09-962-360B-11	Sequence 11, Appl
19	109	100.0	116	4	US-10-802-574-11	Sequence 11, Appl
20	109	100.0	203	3	US-09-942-024-14	Sequence 14, Appl
21	109	100.0	203	3	US-09-942-028-14	Sequence 14, Appl
22	109	100.0	203	4	US-10-261-161-7	Sequence 7, Appl
23	109	100.0	203	5	US-10-917-844-14	Sequence 14, Appl
24	109	100.0	206	3	US-09-942-024-2	Sequence 2, Appl
25	109	100.0	206	3	US-09-942-024-7	Sequence 7, Appl
26	109	100.0	206	3	US-09-942-024-12	Sequence 12, Appl
27	109	100.0	206	3	US-09-942-098-2	Sequence 2, Appl
28	109	100.0	206	3	US-09-942-098-7	Sequence 7, Appl


```
QY 2 ADSNKTTRIDEANQRATKMLGSG 23
Db 12 ADSNKTTRIDEANQRATKMLGSG 33

RESULT 7
US-09-942-098-37
; Sequence 37, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: FRET Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-098-37

Query Match 100.0%; Score 109; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTTRIDEANQRATKMLGSG 23
Db 12 ADSNKTTRIDEANQRATKMLGSG 33

RESULT 8
US-09-942-098-38
; Sequence 38, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: FRET Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-098-38

Query Match 100.0%; Score 109; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTTRIDEANQRATKMLGSG 23
Db 12 ADSNKTTRIDEANQRATKMLGSG 33

RESULT 9
US-10-261-161-55
; Sequence 55, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-261-161-55

Query Match 100.0%; Score 109; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTTRIDEANQRATKMLGSG 23
Db 12 ADSNKTTRIDEANQRATKMLGSG 33

RESULT 10
US-10-261-161-59
; Sequence 59, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-261-161-59

Query Match 100.0%; Score 109; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTTRIDEANQRATKMLGSG 23
Db 12 ADSNKTTRIDEANQRATKMLGSG 33

RESULT 11
US-10-261-161-60
; Sequence 60, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-261-161-60
```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:31:39 ; Search time 19.156 Seconds
(without alignments)
103.582 Million cell updates/sec

Title: US-09-942-098-90
Perfect score: 109
Sequence: 1 XADSNKTRIDEANQRATKMLGSGX 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgm2_6/ptodata/1/iaa/5 COMB.pdp.*
2: /cgm2_6/ptodata/1/iaa/6 COMB.pdp.*
3: /cgm2_6/ptodata/1/iaa/H COMB.pdp.*
4: /cgm2_6/ptodata/1/iaa/PCRTUS COMB.pdp.*
5: /cgm2_6/ptodata/1/iaa/RE COMB.pdp.*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	100.0	26	2	US-08-819-286-8
2	109	100.0	37	2	US-08-819-286-4
3	109	100.0	70	1	US-08-760-001-10
4	109	100.0	70	2	US-09-015-960-10
5	109	100.0	70	2	US-09-534-572-10
6	109	100.0	116	2	US-09-962-360B-11
7	109	100.0	206	1	US-08-393-985-18
8	109	100.0	206	2	US-08-819-286-1
9	109	100.0	206	2	US-09-949-016-6311
10	109	100.0	219	2	US-09-949-016-10671
11	103	94.5	116	2	US-09-962-360B-12
12	99	90.8	20	2	US-08-819-286-9
13	89	81.7	24	2	US-09-962-360B-8
14	83	76.1	17	1	US-08-743-894B-1
15	83	76.1	17	1	US-08-743-894B-37
16	80	73.4	17	1	US-08-743-894B-18
17	80	73.4	17	1	US-08-743-894B-43
18	79	72.5	16	1	US-08-743-894B-49
19	79	72.5	17	1	US-08-743-894B-27
20	79	72.5	17	1	US-08-743-894B-30
21	79	72.5	17	1	US-08-743-894B-32
22	79	72.5	17	1	US-08-743-894B-39
23	78	71.6	17	1	US-08-743-894B-19
24	78	71.6	17	1	US-08-743-894B-25
25	78	71.6	17	1	US-08-743-894B-29
26	78	71.6	17	1	US-08-743-894B-42
27	78	71.6	17	1	US-08-743-894B-50

28	77	70.6	17	1	US-08-743-894B-2	Sequence 2, Appli
29	77	70.6	17	1	US-08-743-894B-20	Sequence 20, Appl
30	77	70.6	17	1	US-08-743-894B-24	Sequence 24, Appl
31	77	70.6	17	1	US-08-743-894B-26	Sequence 26, Appl
32	77	70.6	17	1	US-08-743-894B-28	Sequence 28, Appl
33	77	70.6	17	1	US-08-743-894B-31	Sequence 31, Appl
34	77	70.6	17	1	US-08-743-894B-33	Sequence 33, Appl
35	77	70.6	17	1	US-08-743-894B-34	Sequence 34, Appl
36	77	70.6	17	1	US-08-743-894B-36	Sequence 36, Appl
37	77	70.6	17	1	US-08-743-894B-44	Sequence 44, Appl
38	77	70.6	17	1	US-08-743-894B-45	Sequence 45, Appl
39	77	70.6	17	1	US-08-743-894B-46	Sequence 46, Appl
40	75	68.8	17	1	US-08-743-894B-21	Sequence 21, Appl
41	75	68.8	17	1	US-08-743-894B-35	Sequence 35, Appl
42	75	68.8	17	1	US-08-743-894B-47	Sequence 47, Appl
43	75	68.8	17	1	US-08-743-894B-48	Sequence 48, Appl
44	74	67.9	15	1	US-08-743-894B-38	Sequence 38, Appl
45	74	67.9	17	1	US-08-743-894B-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-819-286-8
; Sequence 8, Application US/08819286
; Patent No. 6163074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L., 842
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-8

Query Match 100.0%; Score 109; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTIDEANQRATKMLGSG 23
|||||

Db 5 ADSNKTIDEANQRATKMLGSG 26

RESULT 2
US-08-819-286-4
; Sequence 4, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montcal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-4

Query Match 100.0%; Score 109; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTIDEANQRATKMLGSG 23
Db 16 ADSNKTIDEANQRATKMLGSG 37

RESULT 3
US-08-760-001-10
; Sequence 10, Application US/08760001
; Patent No. 5962637
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA

Query Match 100.0%; Score 109; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 6.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTIDEANQRATKMLGSG 23
Db 49 ADSNKTIDEANQRATKMLGSG 70

RESULT 4
US-09-015-960-10
; Sequence 10, Application US/09015960
; Patent No. 6043042
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,960
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-015-960-10

Query Match 100.0%; Score 109; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 6.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTIDEANQRATKMLGSG 23
DB 49 ADSNKTIDEANQRATKMLGSG 70

RESULT 5

US-09-534-572-10
Sequence 10, Application US/09534572
Patent No. 6337386
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/015,960
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE: 30-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-534-572-10

Query Match 100.0%; Score 109; DB 2; Length 70;

Best Local Similarity 100.0%; Pred. No. 6.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTIDEANQRATKMLGSG 23
DB 49 ADSNKTIDEANQRATKMLGSG 70

RESULT 6

US-09-962-360B-11
Sequence 11, Application US/09962360B
Patent No. 6762280
GENERAL INFORMATION:
/9
APPLICANT: Schmidt, James J.
APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
TITLE OF INVENTION: Neurotoxins
FILE REFERENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US/09/962,360B
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/235,050
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 11
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-09-962-360B-11

Query Match 100.0%; Score 109; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTIDEANQRATKMLGSG 23
DB 94 ADSNKTIDEANQRATKMLGSG 115

RESULT 7

US-08-393-985-18
Sequence 18, Application US/08393985
Patent No. 5693476
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions for Modulation
TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.

; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-393-985-18

Query Match 100.0%; Score 109; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTIDEANQRATKMLGSG 23
Db 185 ADSNKTIDEANQRATKMLGSG 206

RESULT 8
US-08-819-286-1
; Sequence 1, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Moncal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-1

Query Match 100.0%; Score 109; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTIDEANQRATKMLGSG 23
Db 185 ADSNKTIDEANQRATKMLGSG 206

RESULT 9
US-09-949-016-6311
; Sequence 6311, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6311
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6311

Query Match 100.0%; Score 109; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTIDEANQRATKMLGSG 23
Db 185 ADSNKTIDEANQRATKMLGSG 206

RESULT 10
US-09-949-016-10671
; Sequence 10671, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10671
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10671

Query Match 100.0%; Score 109; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTIDEANQRATKMLGSG 23
Db 198 ADSNKTIDEANQRATKMLGSG 219

RESULT 11
US-09-962-360B-12
; Sequence 12, Application US/09962360B

```

; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-9

Query Match          90.8%; Score 99; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 SNKTRIDEANQRATKMLGSG 23
DB       1 SNKTRIDEANQRATKMLGSG 20
        |||||
RESULT 13
US-09-962-360B-8
; Sequence 8, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
;/9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 8
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by Bonty
US-09-962-360B-8

Query Match          81.7%; Score 89; DB 2; Length 24;
Best Local Similarity 85.0%; Pred. No. 4e-08;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 SNKTRIDEANQRATKMLGSG 23
DB       4 SNRTRIDEANQRATKMLGGG 23
        |||
RESULT 14
US-08-743-894B-1
; Sequence 1, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neu
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESS: MCMR-JA Attn: John Moran-Patent Atty
; STREET: USA MRMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0

```

```

; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-743-894B-1

Query Match 76.1%; Score 83; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SNKTRIDEANQRATKML 20
Db 1 SNKTRIDEANQRATKML 17

RESULT 15
US-08-743-894B-37
; Sequence 37, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear

```

```

; FEATURE:
; US-08-743-894B-37

Query Match 76.1%; Score 83; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SNKTRIDEANQRATKML 20
Db 1 SNKTRIDEANQRATKML 17

Search completed: April 3, 2006, 15:33:14
Job time : 19.156 secs

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM protein - protein search, using sw model

Run on: April 3, 2006, 15:27:42 ; Search time 123.743 Seconds
(without alignments)
136.837 Million cell updates/sec

Title: US-09-942-098-90

Perfect score: 109

Sequence: 1 XADSNKTRIDEANQRATKMLGSG 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	100.0	124	2	Q93578 BRARE
2	109	100.0	134	2	Q488b5 tetraodon n
3	109	100.0	143	2	Q9gm34 macaca fasc
4	109	100.0	198	2	Q6pc84 brachydanio
5	109	100.0	203	1	SN25B CARAU
6	109	100.0	203	2	Q93579 brachydanio
7	109	100.0	203	2	Q6pc54 brachydanio
8	109	100.0	204	1	SN25A CARAU
9	109	100.0	204	2	Q705j6 lateolabrax
10	109	100.0	204	2	Q5tz66 brachydanio
11	109	100.0	204	2	Q5tz65 brachydanio
12	109	100.0	206	1	SNP25 CHICK
13	109	100.0	206	1	SNP25 HUMAN
14	109	100.0	206	1	SNP25 MACHU
15	109	100.0	206	1	SNP25 MOUSE
16	109	100.0	206	1	SNP25 PANTR
17	109	100.0	206	1	SNP25 RAT
18	109	100.0	206	2	Q53EM2 HUMAN
19	109	100.0	206	2	Q5U0B5 HUMAN
20	109	100.0	206	2	Q5NVG5 PONPY
21	109	100.0	206	2	Q5NVK3 PONPY
22	109	100.0	206	2	Q5R690 PONPY
23	109	100.0	206	2	Q5R6U7 PONPY
24	109	100.0	206	2	Q4r4u6 macaca fasc
25	109	100.0	236	2	Q4VS09 CARAU
26	105	96.3	204	2	Q6P3L7 BRARE
27	102	93.6	206	2	Q5R505 PONPY
28	95	87.2	206	2	Q640W4 XENLA
29	95	87.2	206	2	Q8AXM1 XENLA
30	95	87.2	206	2	Q8AXM2 XENLA
31	75	68.8	214	2	Q7ZVE4 BRARE

32 71 65.1 212 2 Q8T3S4 LOLPE
33 70 64.2 210 1 SNP25 TORMA
34 69 63.3 230 2 Q4REP6 TETNG
35 66 60.6 204 2 Q8JIS7 XENLA
36 63 57.8 210 1 SNP23 MOUSE
37 63 57.8 210 1 SNP23 RAT
38 63 57.8 221 2 Q9D3L3 MOUSE
39 62 56.9 211 2 Q5R5T6 PONPY
40 61 56.0 137 2 Q66ID7 BRARE
41 61 56.0 186 2 Q4V9B7 BRARE
42 61 56.0 209 2 Q4V9B6 BRARE
43 59 54.1 211 1 SNP23 HUMAN
44 53 48.6 212 2 O01389 HIRME
45 52 47.7 449 2 Q4NI17_9MICC

ALIGNMENTS

RESULT 1
ID Q93578 BRARE PRELIMINARY; PRT; 124 AA.
AC Q93578; 1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Synaptosome-associated protein 25.1 (Fragment).
GN Name-snap25a; Synonyms=Snap;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9057281; Pubmed=9843147;
RX DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNR13.3.CO;2-Z;
RA Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
RA Larhammar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish:
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage.";
RL J. Neurosci. Res. 54:563-573(1998).
DR EMBL; AF091593; AAC64289.1; -; mRNA.
DR HSSP; Q8T3S4; 1L4A.
DR SMR; Q93578; 49-122.
DR Ensembl; ENSDARG0000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002197; HTH_Fis.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR PRINTS; PR01590; HTHFIS.
DR SMART; SM00397; t-SNARE; 1.
DR PROSITE; PS50192; T-SNARE; 1.
DR Synaptosome.
FT NON TER
SQ SEQUENCE 124 AA; 13616 MW; 50E27DBDB33D958C CRC64;

Query Match 100.0%; Score 109; DB 2; Length 124;

Best Local Similarity 100.0%; Pred. No. 3.4e-09; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTRIDEANQRATKMLGSG 23

Db 103 ADSNKTRIDEANQRATKMLGSG 124

RESULT 2

KW Synaptosome.
SQ SEQUENCE 198 AA; 22209 MW; 8PED5099A00B1EC0 CRC64;
Query Match 100.0%; Score 109; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTTRIDEANQATKMLGSG 23
Db 177 ADSNKTTRIDEANQATKMLGSG 198

RESULT 5
SN25B CARAU STANDARD; PRT; 203 AA.
ID SN25B CARAU
AC P36978;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptosomal-associated protein 25B (SNAP-25B).
GN Name=SNAP-B;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP NUCLEOTIDE SEQUENCE.
TX TISSUE=Retina;
RX MEDLINE=94068448; PubMed=8248151;
RA Risinger C., Larhammar D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid Goldfish.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC -!- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of the nerve terminal.
CC -!- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, and piriform cortex, anterior thalamic nuclei, pontine nuclei, and granule cells of the cerebellum.
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

EMBL; L22976; AAA16538.1; -; mRNA.
PIR; I50481; I50481.
HSSP; P13795; 1SFC.
DR SMR; P36978; 7-82, 128-201.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; t-SNARE.
DR Pfam; PF00835; SNARE; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; t-SNARE; 2.
KW Coiled coil; Glycoprotein; Multigene family; Repeat; Synaptosome.
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 137 199 t-SNARE coiled-coil homology 2.
FT COMBIAS 85 92 Cys-rich.
FT CARBOHYD 77 77 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 185 185 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 203 AA; 22664 MW; 8DFBEBDEB37D6D7 CRC64;

Query Match 100.0%; Score 109; DB 1; Length 203;
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTTRIDEANQATKMLGSG 23
Db 182 ADSNKTTRIDEANQATKMLGSG 203

RESULT 6
O93579 BRARE PRELIMINARY; PRT; 203 AA.
ID O93579 BRARE
AC O93579;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein 25.2.
GN Name=snap25b; Synonym=Snap;
OS Brachydanio rerio (Zebrafish)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
TX MEDLINE=99057281; PubMed=9843147;
RX DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNRL13.3.CO;2-Z;
RA Risinger C., Salanek B., Soderberg C., Gates M., Postlethwait J.H., Larhammar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish: comparison of paralogous linkage groups suggests loss of one locus in the mammalian lineage.";
RL J. Neurosci. Res. 54:563-573(1998).
DR EMBL; AF091594; AAC64290.1; -; mRNA.
DR HSSP; P60881; 1JTH.
DR SMR; O93579; 7-82, 128-201.
DR ZFIN; ZDB-GENE-980526-392; snap25b.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; t-SNARE.
DR Pfam; PF00835; SNARE; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; t-SNARE; 2.
KW Synaptosome.
SQ SEQUENCE 203 AA; 22647 MW; 93B759DD0C93F38 CRC64;

Query Match 100.0%; Score 109; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTTRIDEANQATKMLGSG 23
Db 182 ADSNKTTRIDEANQATKMLGSG 203

RESULT 7
O6PC54 BRARE PRELIMINARY; PRT; 203 AA.
ID O6PC54 BRARE
AC O6PC54;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Synaptosome-associated protein 25 b.
GN Name=snap25b;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
TX STRAIN=Wild-type; TISSUE=Eye;
RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RC NUCLEOTIDE SEQUENCE.
RC STRAIN=Wild; TISSUE=Eye;
RA Strauberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059469; AAHS9469.1; -; mRNA.
DR SNR; Q6PC54; 7-82, 128-201.
DR ZFIN; ZDB-GENE-980526-392; snap25b.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS0192; T_SNARE; 2.
KW Synaptosome.
SQ SEQUENCE 203 AA; 22693 MW; 48D759DD0C1179A CRC64;
Query Match 100.0%; Score 109; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ADSNKTIDEANQRATKMLGSG 23
DB 182 ADSNKTIDEANQRATKMLGSG 203
RESULT 8
ID SN25A_CARAU STANDARD; PRT; 204 AA.
AC P36977;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptosomal-associated protein 25A (SNAP-25A).
OS Name=SNAP-A;
GN Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RX MEDLINE=94068448; PubMed=8248151;
RA Rieinger C., Lathnam D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid
RT goldfish.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602 (1993).
CC -1- FUNCTION: May play an important role in the synaptic function of
CC specific neuronal systems. Associates with proteins involved in
CC vesicle docking and membrane fusion.
CC -1- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
CC the nerve terminal.
CC -1- SIMILARITY: Belongs to the SNAP-25 family.
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR EMBL; L22973; AAA16537.1; -; mRNA.
DR PIR; I50480; I50480.
DR HSP; P13795; IN7S.
DR SNR; P36977; 7-83, 129-202.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS0192; T_SNARE; 2.
KW Coiled coil; Multigene family; Repeat; Synaptosome.
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 138 200 t-SNARE coiled-coil homology 2.
FT COMPBIAS 85 92 Cys-rich.
SQ SEQUENCE 204 AA; 22843 MW; 458BBECFCFC09189 CRC64;
Query Match 100.0%; Score 109; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ADSNKTIDEANQRATKMLGSG 23
DB 183 ADSNKTIDEANQRATKMLGSG 204
RESULT 9
ID Q705J6_LATJA PRELIMINARY; PRT; 204 AA.
AC Q705J6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Synaptosomal-associated protein 25.
GN Name=snap-25;
OS Lateolabrax japonicus (Japanese sea perch) (Japanese sea bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Lateolabrax.
OX NCBI_TaxID=8164;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Chen K., Huang X.H.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ619993; CAP04071.1; -; mRNA.
DR SNR; Q705J6; 7-83, 129-202.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS0192; T_SNARE; 2.
SQ SEQUENCE 204 AA; 22842 MW; 8F77B18D591509B2 CRC64;
Query Match 100.0%; Score 109; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ADSNKTIDEANQRATKMLGSG 23
DB 183 ADSNKTIDEANQRATKMLGSG 204

```

RESULT 10
Q5TZ66 BRARE
ID Q5TZ66; BRARE PRELIMINARY; PRT; 204 AA.
AC Q5TZ66;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Synaptosomal-associated protein (SNAP).
GN Name=snap25a; Synonyms=OTTDARF0000005563; ORFNames=DKEYP-8F4.6-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lovell J.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Donaldson S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX465184; CAI21359.1; -; Genomic DNA.
DR EMBL; BX470246; CAI21359.1; -; Genomic DNA.
DR EMBL; BX470246; CAI21359.1; JOINED; Genomic DNA.
DR EMBL; BX465184; CAI21359.1; JOINED; Genomic DNA.
DR SMR; Q5TZ66; 7-83, 129-202.
DR Ensembl; ENSDARG00000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
DR Synaptosome.
KW Synaptosome.
SQ SEQUENCE 204 AA; 22857 MW; B53CF5F3D1C69EA5 CRC64;

Query Match 100.0%; Score 109; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTTRIDEANQRATKMLGSG 23
Db 183 ADSNKTTRIDEANQRATKMLGSG 204

RESULT 11
Q5TZ65 BRARE
ID Q5TZ65; BRARE PRELIMINARY; PRT; 204 AA.
AC Q5TZ65;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Synaptosomal-associated protein (SNAP).
GN Name=snap25a; Synonyms=OTTDARF0000005690; ORFNames=DKEYP-8F4.6-002;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lovell J.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Donaldson S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX465184; CAH69032.1; -; Genomic DNA.
DR EMBL; BX470246; CAI21360.1; -; Genomic DNA.
DR EMBL; BX470246; CAI21360.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69032.1; JOINED; Genomic DNA.

```

```

DR EMBL; BX465184; CAI21360.1; JOINED; Genomic DNA.
DR SMR; Q5TZ65; 7-83, 129-202.
DR Ensembl; ENSDARG00000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
DR Synaptosome.
KW Synaptosome.
SQ SEQUENCE 204 AA; 22878 MW; FBC79AB7015AC0ED CRC64;

Query Match 100.0%; Score 109; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTTRIDEANQRATKMLGSG 23
Db 183 ADSNKTTRIDEANQRATKMLGSG 204

RESULT 12
SNP25 CHICK
ID SNP25 CHICK STANDARD; PRT; 206 AA.
AC P60878; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
DE 25 kDa protein) (Super protein) (SUP).
GN Name=SNAP25; Synonyms=SNAP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM SNAP25B).
RC STRAIN=White leghorn; TISSUE=Retina;
RX MEDLINE=9112e080; PubMed=1992470;
RA Catasas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,
RA Wilson M.C.;
RT "Expression of a conserved cell-type-specific protein in nerve
RT terminals coincides with synaptogenesis."
RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS SNAP25A AND SNAP25B).
RX MEDLINE=93389738; PubMed=8377193;
RA Bark I.C.;
RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon
RT encoding distinct isoforms of the protein."
RL J. Mol. Biol. 233:67-76(1993).
CC -!- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion (By
CC similarity).
CC -!- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1
CC and SNAP25BP. Binds STXBp6. Found in a ternary complex with STX1A
CC and VAMP8 (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60878-1, P13795-1;
CC Sequence=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60878-2, P13795-2;

```

```
CC      Sequence=VSP_010018;
CC      -i- PTM: Palmitoylated (By similarity).
CC      -i- SIMILARITY: Belongs to the SNAP-25 family.
CC      -i- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; M57957; AAA49072.1; -; mRNA.
DR      EMBL; L09253; AAA49070.1; -; Genomic DNA.
DR      EMBL; L09254; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09255; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09259; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09251; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09258; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09250; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09253; AAA49071.1; -; Genomic DNA.
DR      EMBL; L09254; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09257; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09259; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09252; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09258; AAA49071.1; JOINED; Genomic DNA.
DR      EMBL; L09250; AAA49071.1; JOINED; Genomic DNA.
DR      PIR; A37861; A37861.
DR      SMR; P60878; 7-83, 131-204.
DR      InterPro; IPR000928; SNAP-25.
DR      InterPro; IPR000727; T SNARE.
DR      Pfam; PF00835; SNAP-25; 1.
DR      Pfam; PF05739; SNARE; 1.
DR      SMART; SM00397; t-SNARE; 2.
DR      PROSITE; PS0192; T SNARE; 2.
KW      Alternative splicing; Coiled coil; Lipoprotein; Palmitate;
FT      Phosphorylation; Repeat; Synaptosome.
FT      DOMAIN 19 81
FT      DOMAIN 140 202
FT      COMPIAS 85 92
FT      SITE 180 181
FT      MOD_RES 138 138
FT      MOD_RES 187 187
FT      VARSPIC 58 89
FT      FT
FT      FT
FT      FT
SQ      SEQUENCE 206 AA; 23315 MW; FIED2B082A4CB6A6 CRC64;
      Query Match 100.0%; Score 109; DB 1; Length 206;
      Best Local Similarity 100.0%; Pred. No. 5.8e-09;
      Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      QY      2 ADSNKTTRIDEANQRATKMLGSG 23
      DB      185 ADSNKTTRIDEANQRATKMLGSG 206
      RESULT 13
      SNP25 HUMAN STANDARD; PRT; 206 AA.
      AC P60880; P13795; P36974; P70557; P70558; Q81XK3; Q96FW2; Q9BR45;
      DT 01-JAN-1990 (Rel. 13, Created)
      DT 01-FEB-1991 (Rel. 17, Last sequence update)
      DT 13-SEP-2005 (Rel. 48, Last annotation update)
      DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
      DE 25 kDa protein) (Super protein) (SUP).
      GN Name=SNAP25; Synonyms=SNAP;
      OS Homo sapiens (Human).
      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
      OC Homo.
      OX NCBI_TaxID=9606;
      RN [1]
```

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Kzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 11-81 AND 141-202 IN COMPLEX
WITH STX1A, CPLX1 AND VAMP2, AND NMR ANALYSIS.
MEDLINE=21822661; PubMed=11832227; DOI=10.1016/S0896-6273(02)00583-4;
Chen X., Tomchick D.R., Kovrigin E., Arac D., Machius M.,
Suedhof T.C., Rizo J.;
"Three-dimensional structural structure of the complexin/SNARE complex.";
Neuron 33:397-409(2002).
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion.
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
CC SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with
CC STX1A and VAMP8 (By similarity).
CC -1- INTERACTION:
CC QBIUH5:HIP14; NBExp=1; IntAct=EBI-524785, EBI-524753;
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60880-1, P13795-1;
CC Sequence=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60880-2, P13795-2;
CC Sequence=VSP_006186;
CC -1- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus,
CC piriform cortex, anterior thalamic nuclei, pontine nuclei, and
CC granule cells of the cerebellum.
CC -1- PTM: Palmitoylated (By similarity).
CC -1- SIMILARITY: Belongs to the SNAP-25 family.
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
EMBL; L19760; AAC37545.1; -; mRNA.
EMBL; L19761; AAC37546.1; -; mRNA.
EMBL; D21267; BAA22370.1; -; mRNA.
EMBL; AL023913; CAC34534.1; -; Genomic DNA.
EMBL; AL023913; CAC34535.1; -; Genomic DNA.
EMBL; AL023913; CAD56158.1; -; Genomic DNA.
EMBL; AL023913; CAB42860.1; -; Genomic DNA.
EMBL; BC010647; AAH10647.1; -; mRNA.
PIR; I53735; I53735.
PIR; I67823; I67823.
PDB; 1KIL; X-ray; C=11-80, D=141-203.
PDB; 1XTG; X-ray; B=146-204.
SMR; P60880; 7-83, 131-204.
IntAct; P60880; -;
Ensembl; ENSG00000132639; Homo sapiens.
HGNC; HGNC:11132; SNAP25.
H-InvDB; HIX0015639; -;
MIM; 600322; -;
GO; GO:0007269; P:neurotransmitter secretion; NAS.
DR GO; GO:0001504; P:neurotransmitter uptake; NAS.
DR GO; GO:0050796; P:regulation of insulin secretion; TAS.
DR GO; GO:0007268; P:synaptic transmission; NAS.
DR GO; GO:0016081; P:synaptic vesicle docking during exocytosis; NAS.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.

Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS0192; t-SNARE; 2.
KW 3D-structure; Alternative splicing; Coiled coil; Lipoprotein;
KW Palmitate; Phosphorylation; Repeat; Synaptosome.
FT DOMAIN 19 81
FT t-SNARE coiled-coil homology 1.
FT t-SNARE coiled-coil homology 2.
FT COMPIAS 85 92
FT SITE 180 181
FT MOD_RES 138 138
FT MOD_RES 187 187
FT VARSPPLIC 58 89
FT FT
FT FT
FT HELIX 7 82
FT HELIX 142 201
FT TURN 202 202
SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
Query Match 100.0%; Score 109; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ADSNKTTRIDEANQRATKMLGSG 23
DB 185 ADSNKTTRIDEANQRATKMLGSG 206
RESULT 14
SNP25 MACMU
ID SNP25 MACMU STANDARD; PRT; 206 AA.
AC P60877; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (synaptosomal-associated
DE 25 kDa protein).
GN Name=SNAP25;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Hippocampus;
RA Jensen M.J., Smith L.A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion (By
CC similarity).
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
CC SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with
CC STX1A and VAMP8 (By similarity).
CC -1- PTM: Palmitoylated (By similarity).
CC -1- SIMILARITY: Belongs to the SNAP-25 family.
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
EMBL; AF240770; AAF64477.1; -; mRNA.
DR SMR; P60877; 7-83, 131-204.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.

DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS00192; t_SNARE; 2.
KW Coiled coil; Lipoprotein; Palmitate; Phosphorylation; Repeat;
KW Synaptosome.
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 140 202 t-SNARE coiled-coil homology 2.
FT COMPIAS 85 92 Cys-rich.
FT SITE 180 181 Cleavage (by BONT/E) (By similarity).
FT MOD_RES 138 138 Phosphothreonine (By similarity).
FT MOD_RES 187 187 Phosphoserine (By similarity).
SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
Query Match 100.0%; Score 109; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 5.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ADSNKTTRIDEANORATKMLGSG 23
DB 185 ADSNKTTRIDEANORATKMLGSG 206
RESULT 15
SNP25 MOUSE STANDARD; PRT; 206 AA.
ID SNP25 MOUSE STANDARD; PRT; 206 AA.
AC P60879; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
DE 25 kDa protein) (Super protein) (SUP).
GN Name=Snap25; Synonyms=Snap;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM SNAP-25A).
RC STRAIN=BALB/c;
RX MEDLINE=90078337; PubMed=2592413; DOI=10.1083/jcb.109.6.3039;
RA Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,
RA Bloom P.E., Wilson M.C.;
RT "The identification of a novel synaptosomal-associated protein, SNAP-
RT 25, differentially expressed by neuronal subpopulations.";
RL J. Cell Biol. 109:3039-3052(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM SNAP-25B).
RC STRAIN=ILS, and ISS;
RX MEDLINE=22347237; PubMed=12459461; DOI=10.1016/S0014-5793(02)03629-3;
RA Hepp R., Cabanols J.P., Roche P.A.;
RT "Differential phosphorylation of SNAP-25 in vivo by protein kinase C
RT and protein kinase A.";
RL FEBS Lett. 532:52-56(2002).
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion.
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
CC SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with
CC STX1A and VAMP8 (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60879-1, P13795-1;
CC Sequence=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60879-2, P13795-2;
CC Sequence=VSP_010019;
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25A).
RC STRAIN=C57BL/6; TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rabey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP INTERACTION WITH SNAP25BP.
RX PubMed=10195194; DOI=10.1038/5673;
RA Ilardi J.M., Mochida S., Sheng Z.-H.;
RT "Snapin: a SNARE-associated protein implicated in synaptic
RT transmission.";
RL Nat. Neurosci. 2:119-124(1999).
RN [6]
RP PHOSPHORYLATION SITES THR-138 AND SER-187.
RX MEDLINE=22347237; PubMed=12459461; DOI=10.1016/S0014-5793(02)03629-3;
RA Hepp R., Cabanols J.P., Roche P.A.;
RT "Differential phosphorylation of SNAP-25 in vivo by protein kinase C
RT and protein kinase A.";
RL FEBS Lett. 532:52-56(2002).
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion.
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
CC SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with
CC STX1A and VAMP8 (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60879-1, P13795-1;
CC Sequence=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60879-2, P13795-2;
CC Sequence=VSP_010019;

```
CC -!- PTM: Palmitoylated (By similarity).
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M22012; AAA61741.1; -; mRNA.
CC EMBL; AF483516; AAL90790.1; -; mRNA.
CC EMBL; AF483517; AAL90791.1; -; mRNA.
CC EMBL; AK078038; BAC37105.1; -; mRNA.
CC EMBL; BC018249; AAH18249.1; -; mRNA.
CC EMBL; A33623; A33623.
CC PIR; A33623; A33623.
CC PDB; 2BU0; Model; C=18-82, D=139-206.
CC SMR; P60879; 7-83, 131-204.
CC Ensembl; ENSMUSG0000027273; Mus musculus.
CC MGI; MGI-98331; Snap25.
CC GO; GO:0005886; C:plasma membrane; TAS.
CC GO; GO:0000149; F:SNARE binding; IDA.
CC GO; GO:0007269; P:neurotransmitter secretion; IMP.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T-SNARE.
CC Pfam; PF00835; SNAP-25_1.
CC Pfam; PF05739; SNARE; 1.
CC SMART; SM00397; t-SNARE; 2.
CC PROSITE; PS50192; T-SNARE; 2.
CC 3D-structure; Alternative splicing; Coiled coil; Lipoprotein;
CC Palmitate; Phosphorylation; Repeat; Synaptosome.
CC t-SNARE coiled-coil homology 1.
CC t-SNARE coiled-coil homology 2.
CC Cys-rich.
CC Cleavage (by BONT/E) (By similarity).
CC Phosphothreonine (by PKC and PKA).
CC Phosphoserine (by PKC).
CC ERIEGMDQINKMKEAKNLTDLGKFGGLCV -> DRVVEE
CC GNNHINQDMKEAKNLTDLGKCCGLFI (in isoform
CC SNAP-25a).
CC /FTID=VSP_010019.
SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;

Query Match 100.0%; Score 109; DB 1; Length 206;
Best Local Similarity 100.0%; Pred.No.5.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTIRIDEANQRATKMLGSG 23
   |||||
DB 185 ADSNKTIRIDEANQRATKMLGSG 206

Search completed: April 3, 2006, 15:46:23
Job time : 125.743 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM protein - protein search, using sw model

Run on: April 3, 2006, 15:30:10 ; Search time 12.9908 Seconds
(without alignments)
177.756 Million cell updates/sec

Title: US-09-942-098-90
Perfect score: 109
Sequence: 1 XADSNKTRIDEANQRATKMLGSG 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	203	2 I50481	synapse protein SN
2	109	100.0	204	2 I50480	synapse protein SN
3	109	100.0	206	2 A37861	synaptosomal-assoc
4	109	100.0	206	2 I53735	nerve terminal pro
5	109	100.0	206	2 I67823	nerve terminal pro
6	109	100.0	206	2 A33623	synaptosomal-assoc
7	70	64.2	210	2 I50552	synapse protein -
8	63	57.8	210	2 JC5512	SNARE protein 23 -
9	60.5	55.5	29	2 A49708	synaptosomal-assoc
10	59	54.1	158	2 JC5297	vesicle-membrane f
11	59	54.1	211	2 JC5296	vesicle-membrane f
12	49	45.0	296	2 D87525	conserved hypothe
13	48	44.0	234	2 T65553	hypothetical prote
14	47	43.1	1582	2 AC1153	adhesin homolog lm
15	46	42.2	335	2 T51833	transcription fact
16	46	42.2	1361	2 A29959	DNA-directed RNA p
17	46	42.2	2288	2 T29999	hypothetical prote
18	45	41.3	642	2 G80551	lipoprotein (impor
19	45	41.3	1578	2 AD1512	peptidoglycan boun
20	44	40.4	278	2 ADH356	comE operon protei
21	44	40.4	401	2 E81436	transmembrane tran
22	44	40.4	1578	2 S76238	hypothetical prote
23	44	40.4	1787	2 AG1360	probable tape-meas
24	43	39.4	109	2 C83655	hypothetical prote
25	42.5	39.0	148	2 AB1299	molybdopterin bios
26	42	38.5	83	2 A33854	outer membrane lip
27	42	38.5	219	2 AB1996	hypothetical prote
28	42	38.5	258	2 S38459	replication protei
29	42	38.5	278	2 E72425	dihydropteroate sy

30 42 38.5 420 2 S50562
31 42 38.5 476 1 JC2318
32 42 38.5 657 2 T34037
33 42 38.5 680 2 H70347
34 42 38.5 1056 2 T33167
35 41.5 38.1 181 2 A45422
36 41.5 38.1 181 2 JC4946
37 41 37.6 201 2 T09047
38 41 37.6 261 2 T13220
39 41 37.6 286 2 T16532
40 41 37.6 337 2 AE3039
41 41 37.6 337 2 G98246
42 41 37.6 333 2 T32127
43 41 37.6 438 2 B71963
44 41 37.6 453 2 B48210
45 41 37.6 494 2 S64386

hypothetical prote
angiotensin precur
heat shock 70K pro
outer membrane pro
hypothetical prote
ADP-ribosylation f
ADP-ribosylation f
hypothetical prote
major capsid prote
hypothetical prote
replication protei
repB protein (U809
hypothetical prote
probable outer mem
ezy-1 protein prec
pre-mRNA splicing

ALIGNMENTS

RESULT 1

I50481
synapse protein SNAP-25 - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50481
R;Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Accession: I50481
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-203 <RIS>
A;Cross-references: UNIPROT:P36978; UNIPARC:UPI0000135B03; GB:L22976; NID:G349430; PIDN:?
C;Genetics:
A;Gene: SNAP-25

Query Match 100.0%; Score 109; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTRIDEANQRATKMLGSG 23
Db 182 ADSNKTRIDEANQRATKMLGSG 203

RESULT 2

I50480
synapse protein SNAP-25 - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50480
R;Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Accession: I50480
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-204 <RIS>
A;Cross-references: UNIPROT:P36977; UNIPARC:UPI0000135B02; GB:L22973; NID:G349426; PIDN:?
C;Genetics:
A;Gene: SNAP-25

Query Match 100.0%; Score 109; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTRIDEANQRATKMLGSG 23
Db 183 ADSNKTRIDEANQRATKMLGSG 204

A;Cross-references: GDB:355671; OMIM:600322
A:Map position: 20p11.2-20p11.2

Query Match	100.0%;	Score 109;	DB 2;	Length 206;
Best Local Similarity	100.0%;	Pred. NO. 6.2e-10;		
Matches 22; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 2 ADSNKTRIDEANQRATKMLGSG 23
|||
Dh 185 ADSNKTRIDEANQRATKMLGSG 208

RESULT 6
A33623
synaptosomal-associated 25K protein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 09-Jul-2004
C/Accession: A33623

J. Cell Biol. 109, 3039-3052, 1989.
 J. Royer, G.A.; Higgins, G.A.; Hart, K.A.; Battenberg, E.; Birringre, M.; Snopce, S.
 A. Title: The identification of a novel synaptosomal-associated protein, SNAP-25.
 A. Reference number: A33623; MUID:9007833; PMID:2592413

A;Accession: A33623
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 [GOV](#)

```

Query Match      100.0%; Score 109; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy      2 ADSNKTTRIDEANQRATKMLGSG 23
      ++++++

```

DB 185 ADSNKRTRIDEANQRATKMLGSG 206

RESULT 7

I50552
synapse protein - marbled electric ray
C;Species: Torpedo marmorata (marbled torpedo)
C;Date: 13-Sep-1996 #sequence_revision: 1

J. Biol. Chem. 268, 24408-24414, 1993
 A: Title: Evolutionary conservation of synaptosome-associated protein 25 kDa
 A: Reference number: A49513; MUID:94043281; PMID:8226991
 A: Accession: I50552
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: mRNA

RESULT 3
A37861
synaptosomal-associated 25K protein - chicken
C/Species: Gallus gallus (chicken)
C/Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
C/Accession: A37861
R/Catsicas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A/Title: Expression of a conserved cell-type-specific protein in nerve terminals coincides with the expression of a specific isoform of synaptophysin in the developing chick
A/Reference number: A37861; MUID:91136080; PMID:1992470

A;Accession: A3/801
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <CAT>
A;Cross-references: UNIPROT:P60878; UNIPARC:UPI00000001103; GB:M57957; NID:g212673; PIDN:
Query Match 100.0% Score 109; DB 2: Length 206;

Best Local Similarity 100.0%; Predicted
Matches 22; Conservative 0; Missed

Db 185 ADSNKTRIDEANQRATKMLGSG 206

RESULT 4
I53735
nerve terminal protein - human

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I53735
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994

A;Title: Human CDNA clones encoding two
A;Reference number: I53735; MUID:9415621
A;Accession: I53735
A;Status: preliminary; translated from C

A/Residues: 1-200 (K25)
A/Cross-references: UNIPROT:P60880; UNIPARC:UPI000002B3DD; GB:L19760; NID:g307425; PDB:
C:Genetics:
A/Gene: GDB:SNAP
A/Cross-references: GDB:355671; OMIM:600322
A/Map position: 20p11.2-20p11.2

Query Match	100.0%	Score 109;	DB 2;	Length 206;
Best Local Similarity	100.0%;	Pred. No. 6.2e-10;		
Matches 22; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy 2 ADSNKTRIDEANQRATKMLSG 23
Db 185 ADSNKTRIDEANQRATKMLSG 206

A;Molecule type: mRNA
A;Residues: 1-210 <ARA>
A;Cross-references: UNIPROT:O09044; UNIPARC:UPI000002285C; DDBJ:AB000822; NID:92189950;
C;Comment: This protein is involved in the insulin-induced translocation of vesicles con

Query Match 57.8%; Score 63; DB 2; Length 210;
Best Local Similarity 61.9%; Pred. No. 0.015;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ADSNKTTRIDEANQRATKMLGS 22
Db 190 ADTNKTRIDIANARAKKLIDS 210

RESULT 9
A49708
synaptosomal-associated 25K protein - rat (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 12-Jun-1998
C;Accession: A49708
R;Binz, T.; Blasi, J.; Yamaaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.;
J. Biol. Chem. 269, 1617-1620, 1994
A;Title: Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.
A;Reference number: A49708; MUID:94124495; PMID:8294407
A;Accession: A49708
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-29 <BIN>
A;Cross-references: UNIPARC:UPI000017C9D4

Query Match 55.5%; Score 60.5; DB 2; Length 29;
Best Local Similarity 68.2%; Pred. No. 0.0046;
Matches 15; Conservative 0; Mismatches 0; Indels 7; Gaps 1;

Qy 2 ADSNKTTRIDEANQRATKMLGS 23
Db 15 ADSNKT-----RATKMLGS 29

RESULT 10
JC5297
vesicle-membrane fusion protein SNAP-23B - human
C;Species: Homo sapiens (man)
C;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: JC5297
R;Mollinedo, F.; Lazo, P.A.
Biochem. Biophys. Res. Commun. 231, 808-812, 1997
A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23 i
A;Reference number: JC5296; MUID:97224437; PMID:9070898
A;Accession: JC5297
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-158 <MOI>
A;Cross-references: UNIPROT:O00161; UNIPARC:UPI000002B3DC; GB:Y09568; NID:91924943; PIDN
A;Experimental source: neutrophils
C;Comment: This protein is involved in regulating exocytosis in human neutrophils, a cen

Query Match 54.1%; Score 59; DB 2; Length 158;
Best Local Similarity 57.1%; Pred. No. 0.05;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ADSNKTTRIDEANQRATKMLGS 22
Db 138 ADTNKTRIDIANARAKKLIDS 158

RESULT 11
JC5296
vesicle-membrane fusion protein SNAP-23A - human
C;Species: Homo sapiens (man)
C;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: JC5296
R;Mollinedo, F.; Lazo, P.A.

Biochem. Biophys. Res. Commun. 231, 808-812, 1997
A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23 ir
A;Reference number: JC5296; MUID:97224437; PMID:9070898
A;Accession: JC5296
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-211 <MOL>
A;Cross-references: UNIPROT:O00161; UNIPARC:UPI0000000A2C; GB:Y09567; NID:91924941; PIDN:
C;Comment: This protein is involved in regulating exocytosis in human neutrophils, a cent

Query Match 54.1%; Score 59; DB 2; Length 211;
Best Local Similarity 57.1%; Pred. No. 0.068;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ADSNKTTRIDEANQRATKMLGS 22
Db 191 ADTNKTRIDIANARAKKLIDS 211

RESULT 12
D87525
conserved hypothetical protein CC2229 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D87525
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87525
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-296 <STO>
A;Cross-references: UNIPROT:Q9A665; UNIPARC:UPI00000C765E; GB:AE005673; NID:913423736; P
C;Genetics:
A;Gene: CC2229

Query Match 45.0%; Score 49; DB 2; Length 296;
Best Local Similarity 55.6%; Pred. No. 4;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 6 KTRIDEANQRATKMLGS 23
Db 247 KENVDMANQLKTLGSG 264

RESULT 13
T26553
hypothetical protein Y22F5A.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26553
R;Gardner, A.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z20231
A;Accession: T26553
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-234 <WIL>
A;Cross-references: UNIPROT:O62414; UNIPARC:UPI0000164256; EMBL:AL021479; PIDN:CAAL16332.3
A;Experimental source: clone Y22F5A
C;Genetics:
A;Gene: CESP:Y22F5A.3
A;Map position: 5
A;Introns: 51/3; 82/1; 165/2; 213/3

Query Match 44.0%; Score 48; DB 2; Length 234;
Best Local Similarity 42.1%; Pred. No. 4.4;
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ADSNKTTRIDEANQRATKML 20

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:27:08 ; Search time 123.083 Seconds
(without alignments)
85.675 Million cell updates/sec

Title: US-09-942-098-90
Perfect score: 109
Sequence: 1 XADSNKTRIDEANQRATKMLGSCX 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1980s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	24	AAE36735	Aae36735 Fret subs
2	109	100.0	24	ABW01791	Abw01791 FRET subs
3	109	100.0	26	AAW30099	Aaw30099 Neurotran
4	109	100.0	33	AAE36682	Aae36682 Goldfish
5	109	100.0	33	AAE36683	Aae36683 Goldfish
6	109	100.0	33	AAE36678	Aae36678 SNAP-25 p
7	109	100.0	33	ABW01739	Abw01739 Goldfish
8	109	100.0	33	ABW01734	Abw01734 Mouse SNA
9	109	100.0	33	ABW01738	Abw01738 Goldfish
10	109	100.0	33	ADM97054	Adm97054 Botulinum
11	109	100.0	33	ADM97053	Adm97053 Botulinum
12	109	100.0	33	ADM97049	Adm97049 Botulinum
13	109	100.0	33	AEA14927	Aea14927 Goldfish
14	109	100.0	33	AEA14923	Aea14923 SNAP-25 s
15	109	100.0	33	AEA14928	Aea14928 Goldfish
16	109	100.0	37	AAW30097	Aaw30097 Neurotran
17	109	100.0	70	AAE36823	Aae36823 SNAP-25 r
18	109	100.0	86	AAE15584	Aab15584 Human SNA
19	109	100.0	86	ADP13169	Adp13169 SNAP 25 p
20	109	100.0	114	AAE15002	Aea15002 Clostridi
21	109	100.0	116	AAO15165	Aao15165 Clostridi
22	109	100.0	200	ADN11044	Adn11044 Murine SN
23	109	100.0	203	ABW01715	Abw01715 Goldfish
24	109	100.0	203	ADM97001	Adm97001 Goldfish

25	109	100.0	203	9	AEA14904	Aea14904 Goldfish
26	109	100.0	206	2	AAW30103	Aaw30103 Synaptoso
27	109	100.0	206	2	AAW43426	Aaw43426 Mouse syn
28	109	100.0	206	2	AAW79198	Aaw79198 Mouse SNA
29	109	100.0	206	4	AAU00246	Aau00246 Synaptoso
30	109	100.0	206	4	AAU00253	Aau00253 SNARE hom
31	109	100.0	206	4	AAU00252	Aau00252 SNARE hom
32	109	100.0	206	6	AAE36662	Aae36662 Human SNA
33	109	100.0	206	6	AAE36667	Aae36667 Rat VAMP-
34	109	100.0	206	7	ADE54280	Ades4280 Rat Prote
35	109	100.0	206	7	ADE54288	Ades4288 Rat Prote
36	109	100.0	206	7	ADE54276	Ades4276 Rat Prote
37	109	100.0	206	7	ADE54290	Ades4290 Human Pro
38	109	100.0	206	7	ADE54282	Ades4282 Rat Prote
39	109	100.0	206	7	ADE54274	Ades4274 Rat Prote
40	109	100.0	206	7	ADE54286	Ades4286 Human Pro
41	109	100.0	206	7	ADE54284	Ades4284 Rat Prote
42	109	100.0	206	7	ADE54272	Ades4272 Rat Prote
43	109	100.0	206	7	ADE54278	Ades4278 Rat Prote
44	109	100.0	206	7	ABW01703	Abw01703 Human SNA
45	109	100.0	206	7	ABW01708	Abw01708 Rat VAMP-

ALIGNMENTS

RESULT 1
AAE36735
ID AAE36735 standard; peptide; 24 AA.
XX AC AAE36735;
XX 07-AUG-2003 (first entry)
XX Fret substrate peptide #6 used in the invention.
XX Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
XX tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
XX cosmetic.
XX Unidentified.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "Fluorescein-modified Lysine; This residue is
FT given as Xaa in the sequence shown as SEQ ID NO: 90 in
FT the sequence listing of the specification"
FT Modified-site 24
FT /note= "Tetramethylrhodamine-modified Lysine; C-terminal
FT amide; This residue is given as Xaa in the sequence shown
FT as SEQ ID NO: 90 in the sequence listing of the
FT specification"

WO2003020948-A2.

13-MAR-2003.

22-AUG-2002; 2002WO-US027145.

28-AUG-2001; 2001US-00942024.

(ALLR) ALLERGAN INC.

Steward LE, Fernandez-Salas E, Aoki KR;

WPI; 2003-290198/28.

Botulinum serotype A/E substrate useful for assaying protease activity of
botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
toxin recognition sequence that includes a cleavage site.

Example 1; Page 115; 168pp; English.

CC The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridium toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysates, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridium toxin or having one or more symptoms of a
 CC clostridium toxin, to follow activity during production and purification
 CC of clostridium toxin and to assay formulated clostridium toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is fret
 CC substrate peptide used in the exemplification of the invention

XX
 SQ Sequence 24 AA;

Query Match 100.0%; Score 109; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.9e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTTRIDEANQRATKMLGSG 23
 |||||
 Db 2 ADSNKTTRIDEANQRATKMLGSG 23

RESULT 2
 ABW01791
 ID ABW01791 standard; peptide; 24 AA.

XX AC ABW01791;
 XX DT 12-FEB-2004 (first entry)
 XX DE FRET substrate #4 to analyse proteolytic activity of botulinum toxin.
 XX KW Clostridium toxin; protease activity; tetanus toxin; botulinum toxin;
 XX KW FRET; fluorescence resonance energy transfer.
 XX OS Unidentified.

Key Location/Qualifiers
 FT Modified-site 1 /note= "Fluoresceinated lysine"
 FT Modified-site 24 /note= "Tetramethylrhodamine labelled lysine; C-terminal
 FT amide"
 XX US2003143651-A1.

XX 31-JUL-2003.
 XX 28-AUG-2001; 2001US-00942098.
 XX 28-AUG-2001; 2001US-00942098.
 XX (STEW/) STEWARD L E.
 XX (FERN/) FERNANDEZ-SALAS E.
 XX (AOKI/) AOKI K R.
 XX Steward LE, Fernandez-Salas E, Aoki KR;
 XX WPI; 2003-829791/77.
 XX Determining clostridium toxin protease activity, by treating sample with
 XX clostridium substrate with donor fluorophore, acceptor, toxin recognition
 XX sequence, under conditions which exhibit resonance energy transfer.

XX Example 1; Page 29; Opp; English.
 XX The present invention provides clostridium toxin substrates useful in
 XX assaying for the protease activity of any clostridium toxin including
 XX toxins of all serotypes as well as tetanus toxins. The present sequence
 XX is FRET (fluorescence resonance energy transfer) substrate to analyse
 XX proteolytic activity of botulinum toxin. This substrate is used in the
 XX exemplification of the invention

XX SQ Sequence 24 AA;

Query Match 100.0%; Score 109; DB 7; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.9e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTTRIDEANQRATKMLGSG 23
 |||||
 Db 2 ADSNKTTRIDEANQRATKMLGSG 23

RESULT 3
 AAW30099
 ID AAW30099 standard; peptide; 26 AA.

XX AC AAW30099;
 XX DT 06-APR-1998 (first entry)
 XX DE Neurotransmitter secretion inhibitor #3.
 XX KW Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
 XX KW excitation-secretory uncoupling peptide; catecholamine secretion;
 XX KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
 XX KW synaptosomal associated protein; SNAP-25.
 XX OS Homo sapiens.
 XX PN WO9734620-A1.
 XX 25-SEP-1997.
 XX 18-MAR-1997; 97WO-US004393.
 XX 18-MAR-1996; 96US-0013599P.
 XX (REGC) UNIV CALIFORNIA.
 XX Montal M;
 XX WPI; 1997-479986/44.

XX Excitation-secretory uncoupling peptide(s) for inhibiting
 XX neuro:transmitter release - used particularly for treating muscle
 XX spasticity, and for delivering drugs specifically to neural cells.
 XX Claim 13; Page 31; 61pp; English.

XX This sequence corresponds to residues 181-206 of the human 25 kD
 XX synaptosomal associated protein (SNAP-25), and is an inhibitory agent of
 XX the invention. The agents of the invention inhibit secretion of
 XX neurotransmitter from neuronal cells and is an excitation-secretory
 XX uncoupling peptide (I) of at least 20 amino acids (aa) all of which
 XX correspond substantially to any one of AAW30097-W30102, or more generally
 XX any (I) that inhibits 50% of catecholamine secretion from bovine
 XX chromaffin cells at a concentration of 10 microM, especially 0.25 microM,
 XX or less. (I) are used, as a replacement for Clostridium toxin, to inhibit
 XX release of neurotransmitters from synaptic vesicles, specifically for
 XX reducing muscle spasticity. Also (I) may be labelled to allow in vivo
 XX imaging of intracellular distribution of (I). Compounds for delivering
 XX the drug to neural cells provide targeted drug delivery, e.g. of
 XX substance P to brain tumours for induction of apoptosis. Unlike the
 XX neurotoxins, (I) are not toxic or immunogenic and are more readily

CC available. Their therapeutic effect lasts for several days or weeks, so
 CC lower doses or less frequent treatments are required
 XX Sequence 26 AA;
 SQ Query Match 100.0%; Score 109; DB 2; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 ADSNKTRIDEANQRATKMLGSG 23
 |||||
 Db 5 ADSNKTRIDEANQRATKMLGSG 26
 |||||
 RESULT 4
 AAE36682
 ID AAE36682 standard; peptide; 33 AA.
 XX AAE36682;
 AC
 XX 07-AUG-2003 (first entry)
 DT Goldfish SNAP-25A peptide.
 DE Goldfish; clostridium toxin; protease activity; botulinum toxin; BoNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW TeNT; cosmetic.
 XX Carassius auratus.
 XX OS
 XX FH Key Location/Qualifiers
 FT Cleavage-site 7..8 /note= "BoNT/E sensitive cleavage site"
 FT Cleavage-site 24..25 /note= "BoNT/A sensitive cleavage site"
 FT Cleavage-site 25..26 /note= "BoNT/C sensitive cleavage site"
 FT
 XX WO2003020948-A2.
 XX 13-MAR-2003.
 XX 22-AUG-2002; 2002WO-US027145.
 XX 28-AUG-2001; 2001US-00942024.
 XX (ALLR) ALLERGAN INC.
 XX Steward LE, Fernandez-Salas E, Aoki KR;
 XX WPI; 2003-290198/28.
 DR Botulinum serotype A/E substrate useful for assaying protease activity of
 PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 PT toxin recognition sequence that includes a cleavage site.
 XX Disclosure; Page 42; 168pp; English.
 CC The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for

CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is goldfish
 CC SNAP-25A peptide used in the invention
 XX Sequence 33 AA;
 SQ Query Match 100.0%; Score 109; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 ADSNKTRIDEANQRATKMLGSG 23
 |||||
 Db 12 ADSNKTRIDEANQRATKMLGSG 33
 |||||
 RESULT 5
 AAE36683
 ID AAE36683 standard; peptide; 33 AA.
 XX AAE36683;
 AC
 XX 07-AUG-2003 (first entry)
 DT Goldfish SNAP-25B peptide.
 DE Goldfish; clostridium toxin; protease activity; botulinum toxin; BoNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW TeNT; cosmetic.
 XX Carassius auratus.
 XX OS
 XX FH Key Location/Qualifiers
 FT Cleavage-site 7..8 /note= "BoNT/E sensitive cleavage site"
 FT Cleavage-site 24..25 /note= "BoNT/A sensitive cleavage site"
 FT Cleavage-site 25..26 /note= "BoNT/C sensitive cleavage site"
 FT
 XX WO2003020948-A2.
 XX 13-MAR-2003.
 XX 22-AUG-2002; 2002WO-US027145.
 XX 28-AUG-2001; 2001US-00942024.
 XX (ALLR) ALLERGAN INC.
 XX Steward LE, Fernandez-Salas E, Aoki KR;
 XX WPI; 2003-290198/28.
 DR Botulinum serotype A/E substrate useful for assaying protease activity of
 PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 PT toxin recognition sequence that includes a cleavage site.
 XX Disclosure; Page 42; 168pp; English.
 CC The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for

CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is goldfish
 CC SNAP-25B peptide used in the invention
 XX
 SQ Sequence 33 AA;

Query Match 100.0%; Score 109; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTRIDEANQRATKMLGSG 23
 DB 12 ADSNKTRIDEANQRATKMLGSG 33

RESULT 6
 AAE36678
 ID AAE36678 standard; peptide; 33 AA.
 AC AAE36678;
 XX
 XX 07-AUG-2003 (first entry)
 DT SNAP-25 peptide.
 DE

XX Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW cosmetic; mouse; rat.
 XX

OS Homo sapiens.
 OS Mus musculus.
 OS Rattus sp.

XX Key Location/Qualifiers
 FH Cleavage-site 7. .8
 FT /note= "BoNT/E sensitive cleavage site"
 FT Cleavage-site 24. .25
 FT /note= "BoNT/A sensitive cleavage site"
 FT Cleavage-site 25. .26
 FT /note= "BoNT/C sensitive cleavage site"

XX WO2003020948-A2.

XX 13-MAR-2003.

XX 22-AUG-2002; 2002WO-US027145.

XX 28-AUG-2001; 2001US-00942024.

XX (ALLR) ALLERGAN INC.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-290198/28.

XX Botulinum serotype A/E substrate useful for assaying protease activity of
 PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 PT toxin recognition sequence that includes a cleavage site.

XX Disclosure; Page 42; 168pp; English.

XX The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is

CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is SNAP-25
 CC peptide used in the invention
 XX
 SQ Sequence 33 AA;

Query Match 100.0%; Score 109; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTRIDEANQRATKMLGSG 23
 DB 12 ADSNKTRIDEANQRATKMLGSG 33

RESULT 7
 ABW01739
 ID ABW01739 standard; peptide; 33 AA.
 AC ABW01739;
 XX

XX 12-FEB-2004 (first entry)
 DT Goldfish SNAP-25B BoNT/A cleavage site peptide.
 DE

XX Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
 KW goldfish.
 KW Carassius auratus.
 OS

XX US2003143651-A1.
 XX 31-JUL-2003.

XX 28-AUG-2001; 2001US-00942098.
 XX 28-AUG-2001; 2001US-00942098.

XX (STEW/) STEWARD L E.
 XX (FERN/) FERNANDEZ-SALAS E.
 XX (AOKI/) AOKI K R.

XX Steward LE, Fernandez-Salas E, Aoki KR;
 XX WPI; 2003-829791/77.

XX Determining clostridial toxin protease activity, by treating sample with
 PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
 PT sequence, under conditions which exhibit resonance energy transfer.
 XX Disclosure; Page 11; 0pp; English.
 XX The present invention provides clostridial toxin substrates useful in
 CC assaying for the protease activity of any clostridial toxin including
 CC toxins of all serotypes as well as tetanus toxins. The present sequence
 CC is goldfish SNAP-25B BoNT/A (botulinum neurotoxin serotype A) cleavage
 CC site peptide
 XX
 SQ Sequence 33 AA;

Query Match 100.0%; Score 109; DB 7; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTIDEANQRATKMLGSG 23
 Db 12 ADSNKTIDEANQRATKMLGSG 33

RESULT 8
 ABW01734
 ID ABW01734 standard; peptide; 33 AA.
 AC ABW01734;
 XX 12-FEB-2004 (first entry)
 DT Mouse SNAP-25 BoNT/A cleavage site peptide #1.
 DE Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
 KW mouse.
 KM Mus musculus.
 XX US2003143651-A1.
 PN 31-JUL-2003.
 XX 28-AUG-2001; 2001US-00942098.
 PP 28-AUG-2001; 2001US-00942098.
 XX 28-AUG-2001; 2001US-00942098.
 PR (STEW/) STEWARD L E.
 XX (PERN/) FERNANDEZ-SALAS E.
 PA (AOKI/) AOKI K R.
 PI Steward LE, Fernandez-Salas E, Aoki KR;
 XX WPI; 2003-829791/77.
 DR Determining clostridial toxin protease activity, by treating sample with
 XX clostridial substrate with donor fluorophore, acceptor, toxin recognition
 PT sequence, under conditions which exhibit resonance energy transfer.
 PT Disclosure; Page 11; Opp; English.
 PS The present invention provides clostridial toxin substrates useful in
 XX assaying for the protease activity of any clostridial toxin including
 CC toxins of all serotypes as well as tetanus toxins. The present sequence
 CC is goldfish SNAP-25 BoNT/A (botulinum neurotoxin serotype A) cleavage
 CC site peptide
 XX Sequence 33 AA;
 SQ Query Match 100.0%; Score 109; DB 7; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTIDEANQRATKMLGSG 23
 Db 12 ADSNKTIDEANQRATKMLGSG 33

RESULT 9
 ABW01738
 ID ABW01738 standard; peptide; 33 AA.
 AC ABW01738;
 XX 12-FEB-2004 (first entry)
 DT Goldfish SNAP-25A BoNT/A cleavage site peptide.
 DE Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
 KW goldfish.
 XX

OS Carassius auratus.
 XX US2003143651-A1.
 PN 31-JUL-2003.
 PD 28-AUG-2001; 2001US-00942098.
 XX 28-AUG-2001; 2001US-00942098.
 PF (STEW/) STEWARD L E.
 XX (PERN/) FERNANDEZ-SALAS E.
 PA (AOKI/) AOKI K R.
 PI Steward LE, Fernandez-Salas E, Aoki KR;
 XX WPI; 2003-829791/77.
 DR Determining clostridial toxin protease activity, by treating sample with
 XX clostridial substrate with donor fluorophore, acceptor, toxin recognition
 PT sequence, under conditions which exhibit resonance energy transfer.
 PT Disclosure; Page 11; Opp; English.
 PS The present invention provides clostridial toxin substrates useful in
 XX assaying for the protease activity of any clostridial toxin including
 CC toxins of all serotypes as well as tetanus toxins. The present sequence
 CC is goldfish SNAP-25A BoNT/A (botulinum neurotoxin serotype A) cleavage
 CC site peptide
 XX Sequence 33 AA;
 SQ Query Match 100.0%; Score 109; DB 7; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ADSNKTIDEANQRATKMLGSG 23
 Db 12 ADSNKTIDEANQRATKMLGSG 33

RESULT 10
 ADM97054
 ID ADM97054 standard; peptide; 33 AA.
 AC ADM97054;
 XX 01-JUL-2004 (first entry)
 DT Botulinum toxin substrate recognition sequence #39.
 DE clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.
 XX Carassius auratus.
 OS WO2004029576-A2.
 XX 08-APR-2004.
 PD 04-SEP-2003; 2003WO-US028092.
 XX 27-SEP-2002; 2002US-00261161.
 PR (ALLR) ALLERGAN INC.
 XX Fernandez-Salas E, Steward LE, Aoki KR;
 PI WPI; 2004-340456/31.
 DR Determining clostridial toxin activity, comprises contacting cell with
 XX sample comprising substrate with donor fluorophore, acceptor and
 PT recognition sequence, exciting fluorophore, and determining resonance
 PT energy transfer of contacted cell.

XX Disclosure; SEQ ID NO 60; 188pp; English.

XX

CC The invention relates to a method of determining (M1) clostridial toxin activity, comprising contacting cell with sample comprising clostridial toxin substrate with donor fluorophore (F), acceptor (A) with an absorbance spectrum overlapping emission spectrum of fluorophore clostridial toxin recognition sequence with cleavage site intervening between (F) and (A), where under appropriate conditions resonance transfer is exhibited between fluorophore and acceptor, exciting the donor fluorophore, and determining resonance energy transfer of the contacted cell relative to a control cell, where a difference in resonance energy transfer of the contacted cell as compared to the control cell is indicative of clostridial toxin activity. (M1) is useful for determining clostridial toxin activity, where the sample is a crude cell lysate, isolated clostridial toxin, formulated clostridial toxin product, BOTOX or food. (M1) is an automated high-throughput assay. (M1) reduces the need for animal toxicity studies and serves to analyze multiple toxin functions such as binding a cellular uptake of the toxin, translocation into the cell cytosol and protease activity. In the method M1, the clostridial toxin substrate is a botulinum toxin substrate selected from a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G or TeNT substrate comprising a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G or TeNT recognition sequence. This sequence corresponds to a recognition sequence for a botulinum toxin used as the clostridial toxin substrate.

XX

XX Sequence 33 AA;

Query Match 100.0%; Score 109; DB 8; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTIDEANQRATKMLGSG 23
 |||||

DB 12 ADSNKTIDEANQRATKMLGSG 33

RESULT 11

ID ADM97053

XX ADM97053 standard; peptide; 33 AA.

AC ADM97053;

XX

DT 01-JUL-2004 (first entry)

XX

DE Botulinum toxin substrate recognition sequence #38.

XX

KW clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.

XX

OS Carassius auratus.

XX

PN WO2004029576-A2.

XX

PD 08-APR-2004.

XX

PF 04-SEP-2003; 2003WO-US028092.

XX

PR 27-SEP-2002; 2002US-00261161.

XX

PA (ALLR) ALLERGAN INC.

XX

PI Fernandez-Salas E, Steward LE, Aoki KR;

XX

DR WPI; 2004-340456/31.

XX

PT Determining clostridial toxin activity, comprises contacting cell with sample comprising substrate with donor fluorophore, acceptor and recognition sequence, exciting fluorophore, and determining resonance energy transfer of contacted cell.

XX

PS Disclosure; SEQ ID NO 59; 188pp; English.

XX

CC The invention relates to a method of determining (M1) clostridial toxin activity, comprising contacting cell with sample comprising clostridial toxin substrate with donor fluorophore (F), acceptor (A) with an absorbance spectrum overlapping emission spectrum of fluorophore clostridial toxin recognition sequence with cleavage site intervening between (F) and (A), where under appropriate conditions resonance transfer is exhibited between fluorophore and acceptor, exciting the donor fluorophore, and determining resonance energy transfer of the contacted cell relative to a control cell, where a difference in resonance energy transfer of the contacted cell as compared to the control cell is indicative of clostridial toxin activity. (M1) is useful for determining clostridial toxin activity, where the sample is a crude cell lysate, isolated clostridial toxin, formulated clostridial toxin product, BOTOX or food. (M1) is an automated high-throughput assay. (M1) reduces the need for animal toxicity studies and serves to analyze multiple toxin functions such as binding a cellular uptake of the toxin, translocation into the cell cytosol and protease activity. In the method M1, the clostridial toxin substrate is a botulinum toxin substrate selected from a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G or TeNT substrate comprising a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G or TeNT recognition sequence. This sequence corresponds to a recognition sequence for a botulinum toxin used as the clostridial toxin substrate.

XX

XX Sequence 33 AA;

Query Match 100.0%; Score 109; DB 8; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTIDEANQRATKMLGSG 23
 |||||

DB 12 ADSNKTIDEANQRATKMLGSG 33

RESULT 12

ID ADM97049

XX ADM97049 standard; peptide; 33 AA.

AC ADM97049;

XX

DT 01-JUL-2004 (first entry)

XX

DE Botulinum toxin substrate recognition sequence #34.

XX

KW clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.

XX

OS Mus musculus.

XX

PN WO2004029576-A2.

XX

PD 08-APR-2004.

XX

PF 04-SEP-2003; 2003WO-US028092.

XX

PR 27-SEP-2002; 2002US-00261161.

XX

PA (ALLR) ALLERGAN INC.

XX

PI Fernandez-Salas E, Steward LE, Aoki KR;

XX

DR WPI; 2004-340456/31.

XX

PT Determining clostridial toxin activity, comprises contacting cell with sample comprising substrate with donor fluorophore, acceptor and recognition sequence, exciting fluorophore, and determining resonance energy transfer of contacted cell.

XX

PS Disclosure; SEQ ID NO 55; 188pp; English.

XX

CC The invention relates to a method of determining (M1) clostridial toxin activity, comprising contacting cell with sample comprising clostridial toxin substrate with donor fluorophore (F), acceptor (A) with an

CC absorbance spectrum overlapping emission spectrum of fluorophore
CC clostridial toxin recognition sequence with cleavage site intervening
CC between (F) and (A), where under appropriate conditions resonance
CC transfer is exhibited between fluorophore and acceptor, exciting the
CC donor fluorophore, and determining resonance energy transfer of the
CC contacted cell relative to a control cell, where a difference in
CC resonance energy transfer of the contacted cell as compared to the
CC control cell is indicative of clostridial toxin activity. (M1) is useful
CC for determining clostridial toxin activity, where the sample is a crude
CC cell lysate, isolated clostridial toxin, formulated clostridial toxin
CC product, BOTOX or food. (M1) is an automated high-throughput assay. (M1)
CC reduces the need for animal toxicity studies and serves to analyze
CC multiple toxin functions such as binding a cellular uptake of the toxin,
CC translocation into the cell cytosol and protease activity. In the method
CC M1, the clostridial toxin substrate is a botulinum toxin substrate
CC selected from a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G
CC or TeNT substrate comprising a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E,
CC BONT/F, BONT/G or TeNT recognition sequence. This sequence corresponds to
CC a recognition sequence for a botulinum toxin used as the clostridial
CC toxin substrate.
XX
SQ Sequence 33 AA;

Query Match 100.0%; Score 109; DB 8; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTIDEANQRATKMLGSG 23
DB 12 ADSNKTIDEANQRATKMLGSG 33

RESULT 13
AEA14927
ID AEA14927 standard; peptide; 33 AA.

AC AEA14927;
XX 14-JUL-2005 (first entry)

DT Goldfish SNAP-25 substrate BoNT recognition sequence, SEQ ID NO: 37.

DE Neurotoxin; fluorescence; SNAP-25; botulinum toxin.

KW Carassius auratus.

OS US2005100973-A1.

XX 12-MAY-2005.

XX 13-AUG-2004; 2004US-00917844.

XX 28-AUG-2001; 2001US-00942098.

XX (ALLR) ALLERGAN SALES INC.

XX Steward LE, Gilmore MA, Aoki KR;

XX WPI; 2005-365632/37.

XX Determining clostridial toxin protease activity, by treating sample with

XX tagged toxin substrate comprising fluorescent protein, first and second

XX partner of affinity couple and assaying fluorescent cleavage product in

XX treated sample.

XX Disclosure; SEQ ID NO 37; 97pp; English.

XX The present invention relates to a method for determining protease

XX activity of clostridial neurotoxins such as botulinum neurotoxin (BoNT)

XX and tetanus neurotoxin (TeNT). The method involves treating with a

XX sample, in solution phase under conditions suitable for clostridial toxin

XX protease activity, a tagged toxin substrate (e.g. SNAP-25, VAMP,

XX syntaxin) comprising fluorescent protein, first partner of affinity

CC couple and clostridial toxin recognition sequence comprising cleavage
CC site; contacting treated sample with second partner of affinity couple;
CC and assaying presence of fluorescent cleavage product in the treated
CC sample. The present sequence is the goldfish SNAP-25 substrate BONT/A, E,
CC C (botulinum neurotoxin serotypes A, E, C) recognition sequence.
XX
SQ Sequence 33 AA;

Query Match 100.0%; Score 109; DB 9; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTIDEANQRATKMLGSG 23
DB 12 ADSNKTIDEANQRATKMLGSG 33

RESULT 14
AEA14923
ID AEA14923 standard; peptide; 33 AA.

XX AEA14923;

XX 14-JUL-2005 (first entry)

XX SNAP-25 substrate BoNT recognition sequence, SEQ ID NO: 33.

DE Neurotoxin; fluorescence; SNAP-25; botulinum toxin.

KW Homo sapiens.

XX Mus musculus.

XX Rattus sp.

XX US2005100973-A1.

XX 12-MAY-2005.

XX 13-AUG-2004; 2004US-00917844.

XX 28-AUG-2001; 2001US-00942098.

XX (ALLR) ALLERGAN SALES INC.

XX Steward LE, Gilmore MA, Aoki KR;

XX WPI; 2005-365632/37.

XX Determining clostridial toxin protease activity, by treating sample with

XX tagged toxin substrate comprising fluorescent protein, first and second

XX partner of affinity couple and assaying fluorescent cleavage product in

XX treated sample.

XX Disclosure; SEQ ID NO 33; 97pp; English.

XX The present invention relates to a method for determining protease

XX activity of clostridial neurotoxins such as botulinum neurotoxin (BoNT)

XX and tetanus neurotoxin (TeNT). The method involves treating with a

XX sample, in solution phase under conditions suitable for clostridial toxin

XX protease activity, a tagged toxin substrate (e.g. SNAP-25, VAMP,

XX syntaxin) comprising fluorescent protein, first partner of affinity

XX couple and assaying presence of fluorescent cleavage product in the treated

XX sample. The present sequence is the SNAP-25 substrate BONT/A, E, C

XX (botulinum neurotoxin serotypes A, E, C) recognition sequence. This

XX sequence is found in human, mouse and rat.

XX Sequence 33 AA;

XX Query Match 100.0%; Score 109; DB 9; Length 33;

XX Best Local Similarity 100.0%; Pred. No. 2.8e-10;

XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTREIDANQRATKMLGSG 23
Db 12 ADSNKTREIDANQRATKMLGSG 33

RESULT 15

AEA14928

ID AEA14928 standard; peptide; 33 AA.

XX AEA14928;

XX 14-JUL-2005 (first entry)

XX Goldfish SNAP-25 substrate BoNT recognition sequence, SEQ ID NO: 38.

XX Neurotoxin; fluorescence; SNAP-25; botulinum toxin.

XX Carassius auratus.

XX US2005100973-A1.

XX 12-MAY-2005.

XX 13-AUG-2004; 2004US-00917844.

XX 28-AUG-2001; 2001US-00942098.

XX (ALLR) ALLERGAN SALES INC.

XX Steward LE, Gilmore MA, Aoki KR;

XX WPI; 2005-365632/37.

XX Determining clostridial toxin protease activity, by treating sample with
PT tagged toxin substrate comprising fluorescent protein, first and second
PT partner of affinity couple and assaying fluorescent cleavage product in
PT treated sample.

XX Disclosure; SEQ ID NO 38; 97pp; English.

XX The present invention relates to a method for determining protease
CC activity of clostridial neurotoxins such as botulinum neurotoxin (BoNT)
CC and tetanus neurotoxin (TeNT). The method involves treating with a
CC sample, in solution phase under conditions suitable for clostridial toxin
CC protease activity, a tagged toxin substrate (e.g. SNAP-25, VAMP,
CC syntaxin) comprising fluorescent protein, first partner of affinity
CC couple and clostridial toxin recognition sequence comprising cleavage
CC site; contacting treated sample with second partner of affinity couple;
CC and assaying presence of fluorescent cleavage product in the treated
CC sample. The present sequence is the goldfish SNAP-25 substrate BoNT/A, E,
CC C (botulinum neurotoxin serotypes A, E, C) recognition sequence.

SQ Sequence 33 AA;

Query Match 100.0%; Score 109; DB 9; Length 33;

Best Local Similarity 100.0%; Pred. No. 2.8e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADSNKTREIDANQRATKMLGSG 23

Db 12 ADSNKTREIDANQRATKMLGSG 33

Search completed: April 3, 2006, 15:36:55
Job time : 124.249 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:49:32 ; Search time 8.51376 Seconds
(without alignments)
57.210 Million cell updates/sec

Title: US-09-942-098-91
Perfect score: 68
Sequence: 1 XTRIDEANQRATKMLX 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /SID55/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /SID55/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /SID55/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /SID55/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /SID55/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /SID55/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /SID55/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /SID55/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	68	100.0	17	6	US-10-980-346B-6		Sequence 6, Appli
2	68	100.0	17	6	US-10-980-346B-37		Sequence 37, Appl
3	68	100.0	17	6	US-10-947-071-33		Sequence 33, Appl
4	68	100.0	17	6	US-10-948-097-33		Sequence 33, Appl
5	68	100.0	18	6	US-10-947-071-35		Sequence 35, Appl
6	68	100.0	18	6	US-10-948-097-35		Sequence 35, Appl
7	68	100.0	33	6	US-10-947-071-36		Sequence 36, Appl
8	68	100.0	33	6	US-10-947-071-40		Sequence 40, Appl
9	68	100.0	33	6	US-10-947-071-41		Sequence 41, Appl
10	68	100.0	33	6	US-10-948-097-36		Sequence 36, Appl
11	68	100.0	33	6	US-10-948-097-40		Sequence 40, Appl
12	68	100.0	33	6	US-10-948-097-41		Sequence 41, Appl
13	68	100.0	116	7	US-11-195-098-11		Sequence 11, Appl
14	68	100.0	203	6	US-10-947-071-4		Sequence 4, Appli
15	68	100.0	203	6	US-10-948-097-4		Sequence 4, Appli
16	68	100.0	206	6	US-10-947-071-1		Sequence 1, Appli
17	68	100.0	206	6	US-10-947-071-2		Sequence 2, Appli
18	68	100.0	206	6	US-10-948-097-1		Sequence 1, Appli
19	68	100.0	206	6	US-10-948-097-2		Sequence 2, Appli
20	68	100.0	206	7	US-11-169-041-225		Sequence 225, App
21	68	100.0	334	6	US-10-947-071-20		Sequence 20, Appl
22	68	100.0	334	6	US-10-948-097-20		Sequence 20, Appl
23	65	95.6	17	6	US-10-980-346B-38		Sequence 38, Appl
24	65	95.6	17	6	US-10-947-071-61		Sequence 61, Appl
25	65	95.6	17	6	US-10-948-097-61		Sequence 61, Appl

26	65	95.6	22	6	US-10-980-346B-1	Sequence 1, Appli
27	65	95.6	24	7	US-11-195-098-8	Sequence 8, Appli
28	64	94.1	13	6	US-10-947-071-30	Sequence 30, Appl
29	64	94.1	13	6	US-10-948-097-30	Sequence 30, Appl
30	64	94.1	16	6	US-10-947-071-32	Sequence 32, Appl
31	64	94.1	16	6	US-10-948-097-32	Sequence 32, Appl
32	64	94.1	17	6	US-10-947-071-34	Sequence 34, Appl
33	64	94.1	17	6	US-10-947-071-53	Sequence 53, Appl
34	64	94.1	17	6	US-10-947-071-55	Sequence 55, Appl
35	64	94.1	17	6	US-10-947-071-60	Sequence 60, Appl
36	64	94.1	17	6	US-10-948-097-34	Sequence 34, Appl
37	64	94.1	17	6	US-10-948-097-53	Sequence 53, Appl
38	64	94.1	17	6	US-10-948-097-55	Sequence 55, Appl
39	64	94.1	17	6	US-10-948-097-60	Sequence 60, Appl
40	63	92.6	17	6	US-10-947-071-54	Sequence 54, Appl
41	63	92.6	17	6	US-10-947-071-58	Sequence 58, Appl
42	63	92.6	17	6	US-10-947-071-62	Sequence 62, Appl
43	63	92.6	17	6	US-10-948-097-54	Sequence 54, Appl
44	63	92.6	17	6	US-10-948-097-58	Sequence 58, Appl
45	63	92.6	17	6	US-10-948-097-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1

US-10-980-346B-6
; Sequence 6, Application US/10980346B
; Publication No. US20060024763A1
; GENERAL INFORMATION:
; APPLICANT: Los Alamos National Laboratory
; APPLICANT: Schmidt, Jurgen G., et al.
; TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation of Botulinum Neurotoxins
; FILE REFERENCE: S-102,313
; CURRENT APPLICATION NUMBER: US/10/980,346B
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum
; OTHER INFORMATION: Neurotoxin (BoNT)
US-10-980-346B-6

Query Match 100.0%; Score 68; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15
| | | | | | | | | | | | | | |
Db 4 TRIDEANQRATKML 17

RESULT 2

US-10-980-346B-37
; Sequence 37, Application US/10980346B
; Publication No. US20060024763A1
; GENERAL INFORMATION:
; APPLICANT: Los Alamos National Laboratory
; APPLICANT: Schmidt, Jurgen G., et al.
; TITLE OF INVENTION: Mass Spectrometry-Based Methods for Detection and Differentiation of Botulinum Neurotoxins
; FILE REFERENCE: S-102,313
; CURRENT APPLICATION NUMBER: US/10/980,346B
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 17

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by a Botulinum
; OTHER INFORMATION: Neurotoxin (BoNT)
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(17)
; OTHER INFORMATION: amide bound at one end of the peptide
US-10-980-346B-37

Query Match      100.0%; Score 68; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
Db 4 TRIDEANQRATKML 17

RESULT 3
US-10-947-071-33
; Sequence 33, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-33

Query Match      100.0%; Score 68; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
Db 4 TRIDEANQRATKML 17

RESULT 4
US-10-948-097-33
; Sequence 33, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-10-948-097-33

Query Match      100.0%; Score 68; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
Db 4 TRIDEANQRATKML 17

RESULT 5
US-10-947-071-35
; Sequence 35, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-35

Query Match      100.0%; Score 68; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
Db 5 TRIDEANQRATKML 18

RESULT 6
US-10-948-097-35
; Sequence 35, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-35

Query Match      100.0%; Score 68; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
Db 5 TRIDEANQRATKML 18
```

RESULT 7
US-10-947-071-36
; Sequence 36, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-947-071-36

Query Match 100.0%; Score 68; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANORATKML 15
| | | | | | | | | |
Db 17 TRIDEANORATKML 30

RESULT 8
US-10-947-071-40
; Sequence 40, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-40

Query Match 100.0%; Score 68; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANORATKML 15
| | | | | | | | | |
Db 17 TRIDEANORATKML 30

RESULT 9
US-10-947-071-41
; Sequence 41, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella

; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-41

Query Match 100.0%; Score 68; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANORATKML 15
| | | | | | | | | |
Db 17 TRIDEANORATKML 30

RESULT 10
US-10-948-097-36
; Sequence 36, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-948-097-36

Query Match 100.0%; Score 68; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANORATKML 15
| | | | | | | | | |
Db 17 TRIDEANORATKML 30

RESULT 11
US-10-948-097-40
; Sequence 40, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-40

Query Match          100.0%; Score 68; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TRIDEANORATKML 15
Db      17 TRIDEANORATKML 30
|||||
|||||

RESULT 12
US-10-948-097-41
; Sequence 41, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-41

Query Match          100.0%; Score 68; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TRIDEANORATKML 15
Db      17 TRIDEANORATKML 30
|||||
|||||

RESULT 13
US-11-195-098-11
; Sequence 11, Application US/11195098
; Publication No. US20050287622A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/11/195,098
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/802,574
; PRIOR FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 09/962,360
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-L-cysteine
US-11-195-098-11

Query Match          100.0%; Score 68; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TRIDEANORATKML 15
Db      99 TRIDEANORATKML 112
|||||
|||||

RESULT 14
US-10-947-071-4
; Sequence 4, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-4

Query Match          100.0%; Score 68; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TRIDEANORATKML 15
Db      187 TRIDEANORATKML 200
|||||
|||||

RESULT 15
US-10-948-097-4
; Sequence 4, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-4

Query Match          100.0%; Score 68; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TRIDEANORATKML 15
Db      187 TRIDEANORATKML 200
|||||
|||||
```

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANORATKML 15

Db 187 TRIDEANORATKML 200

Search completed: April 3, 2006, 15:58:09
Job time : 8.51376 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:46:49 ; Search time 68.844 Seconds
(without alignments)
97.107 Million cell updates/sec

Title: US-09-942-098-91

Perfect score: 68

Sequence: 1 XTRIDEANQRATKMLX 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_Main.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	16	3	US-09-942-024-91
2	68	100.0	16	3	US-09-942-024-94
3	68	100.0	16	3	US-09-942-098-91
4	68	100.0	16	3	US-09-942-098-94
5	68	100.0	17	3	US-09-942-024-30
6	68	100.0	17	3	US-09-942-098-30
7	68	100.0	17	4	US-10-011-588-2
8	68	100.0	17	4	US-10-261-161-52
9	68	100.0	17	4	US-10-261-161-68
10	68	100.0	17	5	US-10-917-844-30
11	68	100.0	18	3	US-09-942-024-32
12	68	100.0	18	3	US-09-942-098-32
13	68	100.0	18	4	US-10-261-161-54
14	68	100.0	18	5	US-10-917-844-32
15	68	100.0	19	3	US-09-942-024-85
16	68	100.0	19	3	US-09-942-024-92
17	68	100.0	19	3	US-09-942-024-95
18	68	100.0	19	3	US-09-942-098-85
19	68	100.0	19	3	US-09-942-098-92
20	68	100.0	19	3	US-09-942-098-95
21	68	100.0	19	4	US-10-705-857-6
22	68	100.0	21	3	US-09-942-024-89
23	68	100.0	21	3	US-09-942-098-89
24	68	100.0	22	3	US-09-942-024-93
25	68	100.0	22	3	US-09-942-098-93
26	68	100.0	23	3	US-09-942-024-88
27	68	100.0	23	3	US-09-942-098-88

28	68	100.0	24	3	US-09-942-024-90	Sequence 90, Appl
29	68	100.0	24	3	US-09-942-098-90	Sequence 90, Appl
30	68	100.0	33	3	US-09-942-024-33	Sequence 33, Appl
31	68	100.0	33	3	US-09-942-024-37	Sequence 37, Appl
32	68	100.0	33	3	US-09-942-024-38	Sequence 38, Appl
33	68	100.0	33	3	US-09-942-098-33	Sequence 33, Appl
34	68	100.0	33	3	US-09-942-098-37	Sequence 37, Appl
35	68	100.0	33	3	US-09-942-098-38	Sequence 38, Appl
36	68	100.0	33	4	US-10-261-161-55	Sequence 55, Appl
37	68	100.0	33	4	US-10-261-161-59	Sequence 59, Appl
38	68	100.0	33	4	US-10-261-161-60	Sequence 60, Appl
39	68	100.0	33	5	US-10-917-844-33	Sequence 33, Appl
40	68	100.0	33	5	US-10-917-844-37	Sequence 37, Appl
41	68	100.0	33	5	US-10-917-844-38	Sequence 38, Appl
42	68	100.0	86	4	US-10-705-857-4	Sequence 4, Appl
43	68	100.0	114	5	US-10-917-844-112	Sequence 112, Appl
44	68	100.0	116	3	US-09-962-3608-11	Sequence 11, Appl
45	68	100.0	116	4	US-10-802-574-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-942-024-91
; Sequence 91, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 16
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-91

Query Match 100.0%; Score 68; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15
| | | | | | | | | | | | | | |
Db 2 TRIDEANQRATKML 15

RESULT 2
US-09-942-024-94
; Sequence 94, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum

```
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa-DABCYL modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 16
; OTHER INFORMATION: Xaa=EDANS modified glutamate
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
;
US-09-942-024-94

Query Match      100.0%; Score 68; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 TRIDEANQRATKML 15
Db  2 TRIDEANQRATKML 15

RESULT 3
US-09-942-098-91
; Sequence 91, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 16
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
;
US-09-942-098-91

Query Match      100.0%; Score 68; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 TRIDEANQRATKML 15
Db  2 TRIDEANQRATKML 15
```

```
RESULT 4
US-09-942-098-94
; Sequence 94, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa-DABCYL modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 16
; OTHER INFORMATION: Xaa=EDANS modified glutamate
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
;
US-09-942-098-94

Query Match      100.0%; Score 68; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 TRIDEANQRATKML 15
Db  2 TRIDEANQRATKML 15

RESULT 5
US-09-942-024-30
; Sequence 30, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-942-024-30

Query Match      100.0%; Score 68; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 TRIDEANQRATKML 15
Db  4 TRIDEANQRATKML 17

RESULT 6
US-09-942-098-30
```

; Sequence 30, Application US/09942098
 ; Publication No. US20030143651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steward, Lance E.
 ; APPLICANT: Fernandez-Salas, Ester
 ; APPLICANT: Aoki, Kei Roger
 ; TITLE OF INVENTION: Fret Protease Assays For Clostridial Toxins
 ; TITLE OF INVENTION: Toxins
 ; FILE REFERENCE: P-AR 4802
 ; CURRENT APPLICATION NUMBER: US/09/942,098
 ; CURRENT FILING DATE: 2001-08-28
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 30
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 US-09-942-098-30

Query Match 100.0%; Score 68; DB 3; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKML 15
 |||||
 DB 4 TRIDEANORATKML 17

RESULT 7
 US-10-011-588-2
 ; Sequence 2, Application US/10011588
 ; Publication No. US2002016872A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Smith, Leonard
 ; APPLICANT: Jensen, Melody
 ; TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM
 ; TITLE OF INVENTION: NEUROTOXINS AND LIGHT CHAIN FUSION PROTEINS FOR USE IN
 ; TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY
 ; FILE REFERENCE: A34796 067252.0113
 ; CURRENT APPLICATION NUMBER: US/10/011,588
 ; CURRENT FILING DATE: 2002-03-29
 ; PRIOR APPLICATION NUMBER: 09/910,186
 ; PRIOR FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: 09/611,419
 ; PRIOR FILING DATE: 2000-07-06
 ; PRIOR APPLICATION NUMBER: 60/246,744
 ; PRIOR FILING DATE: 2000-11-06
 ; PRIOR APPLICATION NUMBER: 60/311,966
 ; PRIOR FILING DATE: 2001-08-09
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (0)...(0)
 ; OTHER INFORMATION: Residues 187-203 of SNAP-25
 US-10-011-588-2

Query Match 100.0%; Score 68; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKML 15
 |||||
 DB 4 TRIDEANORATKML 17

RESULT 8
 US-10-261-161-52
 ; Sequence 52, Application US/10261161

; Publication No. US20040072270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fernandez-Salas, Ester
 ; APPLICANT: Steward, Lance E.
 ; APPLICANT: Aoki, Kei Roger
 ; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
 ; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
 ; FILE REFERENCE: P-AR 4804
 ; CURRENT APPLICATION NUMBER: US/10/261,161
 ; CURRENT FILING DATE: 2002-09-27
 ; NUMBER OF SEQ ID NOS: 109
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 52
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 US-10-261-161-52

Query Match 100.0%; Score 68; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKML 15
 |||||
 DB 4 TRIDEANORATKML 17

RESULT 9
 US-10-261-161-68
 ; Sequence 68, Application US/10261161
 ; Publication No. US20040072270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fernandez-Salas, Ester
 ; APPLICANT: Steward, Lance E.
 ; APPLICANT: Aoki, Kei Roger
 ; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
 ; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
 ; FILE REFERENCE: P-AR 4804
 ; CURRENT APPLICATION NUMBER: US/10/261,161
 ; CURRENT FILING DATE: 2002-09-27
 ; NUMBER OF SEQ ID NOS: 109
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 68
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic construct
 US-10-261-161-68

Query Match 100.0%; Score 68; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKML 15
 |||||
 DB 4 TRIDEANORATKML 17

RESULT 10
 US-10-917-844-30
 ; Sequence 30, Application US/10917844
 ; Publication No. US20050100973A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steward, Lance E.
 ; APPLICANT: Gilmore, Marcella A.
 ; APPLICANT: Aoki, Kei R.
 ; TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
 ; TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
 ; FILE REFERENCE: 66872-044
 ; CURRENT APPLICATION NUMBER: US/10/917,844
 ; CURRENT FILING DATE: 2004-08-13
 ; PRIOR APPLICATION NUMBER: US 09/942,098

```
/ PRIOR FILING DATE: 2001-08-28
/ NUMBER OF SEQ ID NOS: 113
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 30
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-917-844-30

Query Match      100.0%; Score 68; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
Db 4 TRIDEANQRATKML 17

RESULT 11
US-09-942-024-32
/ Sequence 32, Application US/09942024
/ Publication No. US20030143650A1
/ GENERAL INFORMATION:
/ APPLICANT: Steward, Lance E.
/ APPLICANT: Fernandez-Salas, Ester
/ APPLICANT: Aoki, Kei Roger
/ TITLE OF INVENTION: Fret Protease Assays For Botulinum
/ TITLE OF INVENTION: Serotype A/E Toxins
/ FILE REFERENCE: P-AR 4803
/ CURRENT APPLICATION NUMBER: US/09/942,024
/ CURRENT FILING DATE: 2001-08-28
/ NUMBER OF SEQ ID NOS: 96
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 32
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-942-024-32

Query Match      100.0%; Score 68; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
Db 5 TRIDEANQRATKML 18

RESULT 12
US-09-942-098-32
/ Sequence 32, Application US/09942098
/ Publication No. US20030143651A1
/ GENERAL INFORMATION:
/ APPLICANT: Steward, Lance E.
/ APPLICANT: Fernandez-Salas, Ester
/ APPLICANT: Aoki, Kei Roger
/ TITLE OF INVENTION: Fret Protease Assays For Clostridial
/ TITLE OF INVENTION: Toxins
/ FILE REFERENCE: P-AR 4802
/ CURRENT APPLICATION NUMBER: US/09/942,098
/ CURRENT FILING DATE: 2001-08-28
/ NUMBER OF SEQ ID NOS: 96
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 32
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-942-098-32

Query Match      100.0%; Score 68; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 TRIDEANQRATKML 15
Db 5 TRIDEANQRATKML 18

RESULT 13
US-10-261-161-54
/ Sequence 54, Application US/10261161
/ Publication No. US20040072270A1
/ GENERAL INFORMATION:
/ APPLICANT: Fernandez-Salas, Ester
/ APPLICANT: Steward, Lance E.
/ APPLICANT: Aoki, Kei Roger
/ TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
/ TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
/ FILE REFERENCE: P-AR 4804
/ CURRENT APPLICATION NUMBER: US/10/261,161
/ CURRENT FILING DATE: 2002-09-27
/ NUMBER OF SEQ ID NOS: 109
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 54
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-261-161-54

Query Match      100.0%; Score 68; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
Db 5 TRIDEANQRATKML 18

RESULT 14
US-10-917-844-32
/ Sequence 32, Application US/10917844
/ Publication No. US20050100973A1
/ GENERAL INFORMATION:
/ APPLICANT: Steward, Lance E.
/ APPLICANT: Gilmore, Marcella A.
/ APPLICANT: Aoki, Kei R.
/ TITLE OF INVENTION: GFP-SANP25 Fluorescence Release Assay
/ TITLE OF INVENTION: For Botulinum Neurotoxin Protease Activity
/ FILE REFERENCE: 66872-044
/ CURRENT APPLICATION NUMBER: US/10/917,844
/ CURRENT FILING DATE: 2004-08-13
/ PRIOR APPLICATION NUMBER: US 09/942,098
/ PRIOR FILING DATE: 2001-08-28
/ NUMBER OF SEQ ID NOS: 113
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 32
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-917-844-32

Query Match      100.0%; Score 68; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
Db 5 TRIDEANQRATKML 18

RESULT 15
US-09-942-024-85
/ Sequence 85, Application US/09942024
/ Publication No. US20030143650A1
/ GENERAL INFORMATION:
/ APPLICANT: Steward, Lance E.
```

APPLICANT: Fernandez-Salas, Ester
APPLICANT: Aoki, Kei Roger
TITLE OF INVENTION: Fret Protease Assays For Botulinum
TITLE OF INVENTION: Serotype A/E Toxins
FILE REFERENCE: P-AR 4803
CURRENT APPLICATION NUMBER: US/09/942,024
CURRENT FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 85
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic construct
NAME/KEY: MOD_RES
LOCATION: 1
OTHER INFORMATION: Xaa-fluorescein-modified lysine
NAME/KEY: MOD_RES
LOCATION: 20
OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
NAME/KEY: AMIDATION
LOCATION: (O)...(O)
OTHER INFORMATION: at the C-terminal
US-09-942-024-85

Query Match 100.0%; Score 68; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
| | | | | | | | | | | | | | | | | | | | | |
Db 5 TRIDEANQRATKML 18

Search completed: April 3, 2006, 15:57:05
Job time : 68.844 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:31:39 ; Search time 12.7706 Seconds
(without alignments)
103.582 Million cell updates/sec

Title: US-09-942-098-91

Perfect score: 68
Sequence: 1 XTRIDEANQRATKMLX 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pdp.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pdp.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pdp.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pdp.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pdp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	17	1	US-08-743-894B-1
2	68	100.0	17	1	US-08-743-894B-37
3	68	100.0	20	2	US-08-819-286-9
4	68	100.0	26	2	US-08-819-286-8
5	68	100.0	37	2	US-08-819-286-4
6	68	100.0	70	1	US-08-760-001-10
7	68	100.0	70	2	US-09-015-960-10
8	68	100.0	70	2	US-09-534-572-10
9	68	100.0	116	2	US-09-962-360B-11
10	68	100.0	206	1	US-08-393-985-18
11	68	100.0	206	2	US-08-819-286-1
12	68	100.0	206	2	US-09-949-016-6311
13	68	100.0	219	2	US-09-949-016-10671
14	65	95.6	17	1	US-08-743-894B-2
15	65	95.6	17	1	US-08-743-894B-18
16	65	95.6	17	1	US-08-743-894B-43
17	65	95.6	24	2	US-09-962-360B-8
18	64	94.1	13	2	US-09-976-535A-1
19	64	94.1	16	1	US-08-743-894B-27
20	64	94.1	17	1	US-08-743-894B-49
21	64	94.1	17	1	US-08-743-894B-30
22	64	94.1	17	1	US-08-743-894B-32
23	64	94.1	17	1	US-08-743-894B-39
24	63	92.6	17	1	US-08-743-894B-19
25	63	92.6	17	1	US-08-743-894B-25
26	63	92.6	17	1	US-08-743-894B-29
27	63	92.6	17	1	US-08-743-894B-42

28	63	92.6	17	1	US-08-743-894B-50	Sequence 50, Appl
29	62	91.2	17	1	US-08-743-894B-3	Sequence 3, Appl
30	62	91.2	17	1	US-08-743-894B-20	Sequence 20, Appl
31	62	91.2	17	1	US-08-743-894B-24	Sequence 24, Appl
32	62	91.2	17	1	US-08-743-894B-26	Sequence 26, Appl
33	62	91.2	17	1	US-08-743-894B-28	Sequence 28, Appl
34	62	91.2	17	1	US-08-743-894B-31	Sequence 31, Appl
35	62	91.2	17	1	US-08-743-894B-33	Sequence 33, Appl
36	62	91.2	17	1	US-08-743-894B-34	Sequence 34, Appl
37	62	91.2	17	1	US-08-743-894B-36	Sequence 36, Appl
38	62	91.2	17	1	US-08-743-894B-44	Sequence 44, Appl
39	62	91.2	17	1	US-08-743-894B-45	Sequence 45, Appl
40	62	91.2	17	1	US-08-743-894B-46	Sequence 46, Appl
41	62	91.2	116	2	US-09-962-360B-12	Sequence 12, Appl
42	61	89.7	13	1	US-08-743-894B-16	Sequence 16, Appl
43	61	89.7	14	2	US-09-976-535A-2	Sequence 2, Appl
44	61	89.7	16	1	US-08-743-894B-51	Sequence 51, Appl
45	61	89.7	17	1	US-08-743-894B-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-743-894B-1
; Sequence 1, Application US/08743894B
; Patent No. 5965699

GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MEMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743.894B
; FILING DATE: No. 5965699member 6, 1996

CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear

US-08-743-894B-1
Query Match 100.0%; Score 68; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15
Db 4 TRIDEANQRATKML 17

```
RESULT 2
US-08-743-894B-37
; Sequence 37, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn: John Moran-Patent Atty
; STREET: USA MEMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
US-08-743-894B-37
Query Match 100.0%; Score 68; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15
Db 4 TRIDEANQRATKML 17
|||||

RESULT 3
US-08-819-286-9
; Sequence 9, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; MEDIUM TYPE: Floppy disk
```

```
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-819-286-9
Query Match 100.0%; Score 68; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15
Db 4 TRIDEANQRATKML 17
|||||

RESULT 4
US-08-819-286-8
; Sequence 8, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
```

```
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-819-286-8
Query Match 100.0%; Score 68; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15
Db 10 TRIDEANQRATKML 23

RESULT 5
US-08-819-286-4
; Sequence 4, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-819-286-4
Query Match 100.0%; Score 68; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15
Db 21 TRIDEANQRATKML 34

RESULT 6
US-08-760-001-10
; Sequence 10, Application US/08760001
; Patent No. 5962637
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,001
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-760-001-10
Query Match 100.0%; Score 68; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15
Db 54 TRIDEANQRATKML 67

RESULT 7
US-09-015-960-10
; Sequence 10, Application US/09015960
; Patent No. 6043042
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,960
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-015-960-10

Query Match 100.0%; Score 68; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
Db 54 TRIDEANQRATKML 67

RESULT 8
US-09-534-572-10
; Sequence 10, Application US/09534572
; Patent No. 6337386
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/534,572
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,960
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE: 30-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120003
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-534-572-10

Query Match 100.0%; Score 68; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
Db 54 TRIDEANQRATKML 67

RESULT 9
US-09-962-360B-11
; Sequence 11, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; FILE REFERENCE: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
; US-09-962-360B-11

Query Match 100.0%; Score 68; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
Db 99 TRIDEANQRATKML 112

RESULT 10
US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Scheller, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA

```

; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-393-985-18

```

```

Query Match 100.0%; Score 68; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.00012; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

```

```

QY 2 TRIDEANQRATKML 15
Db 190 TRIDEANQRATKML 203

```

```

RESULT 11
US-08-819-286-1
; Sequence 1, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid

```

```

; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-1
;
Query Match 100.0%; Score 68; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.00012; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

```

```

QY 2 TRIDEANQRATKML 15
Db 190 TRIDEANQRATKML 203

```

```

RESULT 12
US-09-949-016-6311
; Sequence 6311, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6311
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6311

```

```

Query Match 100.0%; Score 68; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.00012; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

```

```

QY 2 TRIDEANQRATKML 15
Db 190 TRIDEANQRATKML 203

```

```

RESULT 13
US-09-949-016-10671
; Sequence 10671, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10671
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10671

```

```
Query Match      100.0%; Score 68; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TRIDEANQRATKML 15
Db      203 TRIDEANQRATKML 216

RESULT 14
US-08-743-894B-2
; Sequence 2, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MRMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
US-08-743-894B-2

Query Match      95.6%; Score 65; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.4e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 TRIDEANQRATKML 15
Db      4 TRIDEANQRATKML 17

RESULT 15
US-08-743-894B-18
; Sequence 18, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MRMC - 504 Scott Street
```

```
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
US-08-743-894B-18

Query Match      95.6%; Score 65; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.4e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 TRIDEANQRATKML 15
Db      4 TRIDEANQRATKML 17

Search completed: April 3, 2006, 15:33:15
Job time : 12.7706 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocollaboration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:27:42 ; Search time 82.4954 Seconds
(without alignments)
136.837 Million cell updates/sec

Title: US-09-942-098-91
Perfect score: 68
Sequence: 1 XTRIDEANQRATKMLX 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	124	2	Q93578 BRARE
2	68	100.0	134	2	Q48b5 brachydanio
3	68	100.0	143	2	Q8885 TETNG
4	68	100.0	198	2	Q8GM34 MACFA
5	68	100.0	203	1	Q6PC84 BRARE
6	68	100.0	203	1	SN25B CARAU
7	68	100.0	203	2	Q93579 BRARE
8	68	100.0	204	1	Q6PC54 BRARE
9	68	100.0	204	2	SN25A CARAU
10	68	100.0	204	2	Q705J6 LATJA
11	68	100.0	204	2	Q5T266 BRARE
12	68	100.0	206	1	SNP25 CHICK
13	68	100.0	206	1	SNP25 HUMAN
14	68	100.0	206	1	SNP25 MACMU
15	68	100.0	206	1	SNP25 MOUSE
16	68	100.0	206	1	SNP25 PANTR
17	68	100.0	206	1	SNP25 RAT
18	68	100.0	206	2	Q53EM2 HUMAN
19	68	100.0	206	2	Q5U0B5 HUMAN
20	68	100.0	206	2	Q5NVG5 PONPY
21	68	100.0	206	2	Q5NVK3 PONPY
22	68	100.0	206	2	Q5R690 PONPY
23	68	100.0	206	2	Q5R6U7 PONPY
24	68	100.0	206	2	Q4R4U6 MACFA
25	68	100.0	236	2	Q4VS09 CARAU
26	64	94.1	204	2	Q6F3L7 BRARE
27	61	89.7	206	2	Q5R505 PONPY
28	55	80.9	214	2	Q7ZVE4 BRARE
29	54	79.4	137	2	Q66ID7 BRARE
30	54	79.4	186	2	Q4V9B7 BRARE
31	54	79.4	206	2	Q640W4 XENLA

32	54	79.4	206	2	Q8AXM1 XENLA	Q8axm1 xenopus lae
33	54	79.4	206	2	Q8AXM2 XENLA	Q8axm2 xenopus lae
34	54	79.4	209	2	Q4V9B6 BRARE	Q4v9b6 brachydanio
35	54	79.4	210	1	SNP25 TORMA	P36976 torpedo mar
36	54	79.4	212	2	Q8T3S4 LOLPE	Q8t3s4 loligo peal
37	53	77.9	230	2	Q4REP6 TETNG	Q4rep6 tetraodon n
38	48	70.6	204	2	Q8JIS7 XENLA	Q8jia7 xenopus lae
39	46	67.6	220	2	Q869G6 LYMST	Q869g6 lymnaea sta
40	45	66.2	83	2	Q85431 PSEFL	Q85431 pseudomonas
41	45	66.2	83	2	Q85439 PSEFL	Q85439 pseudomonas
42	45	66.2	83	2	Q85440 PSETO	Q85440 pseudomonas
43	43	63.2	212	2	O01389 HIRME	O01389 hirudo medi
44	42	61.8	55	2	Q8NCR8 HUMAN	Q8ncr8 homo sapien
45	42	61.8	83	1	OPRI_PSEAE	P11221 pseudomonas

ALIGNMENTS

RESULT 1
ID O93578 BRARE PRELIMINARY; PRT; 124 AA.
AC O93578;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Synaptosome-associated protein 25.1 (Fragment).
GN Name=snap25a; Synonyms=Snap;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=39057281; PubMed=9843147;
RX DOI=10.1002/(SICI)1097-4547(19981201)54:5:563::AID-JNRL13.3.CO;2-Z;
RA Risinger C., Salanek E., Soderberg C., Gates M., Postlethwait J.H.,
RA Larhammer D.;
RT "Cloning of two loci for synapse protein snap25 in zebrafish:
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage.";
RL J. Neurosci. Res. 54:563-573 (1998).
DR EMBL; AF091593; AAC64289.1; -; mRNA.
DR HSP; Q8T3S4; 1L4A.
DR SMR; Q93578; 49-122.
DR Ensembl; ENSDARG0000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002197; HTH_Fis.
DR InterPro; IPR00928; SNAP_25.
DR InterPro; IPR00072; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR PRINTS; PR01590; HTHFIS.
DR SMART; SM00397; t_SNARE; 1.
DR PROSITE; PS50192; T_SNARE; 1.
DR Synaptosome.
KW NON TER
FT
SQ SEQUENCE 124 AA; 13616 MW; 50E27DBB33D958C CRC64;

Query Match 100.0%; Score 68; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15
| | | | | | | | | | | | | | |
Db 108 TRIDEANQRATKML 121
| | | | | | | | | | | | | | |

RESULT 2

KW Synaptosome.
SQ SEQUENCE 198 AA; 22209 MW; 8FED5099A00B1E0C CRC64;

Query Match 100.0%; Score 68; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANORATKML 15
Db 182 TRIDEANORATKML 195

RESULT 5
SN25B CARAU STANDARD; PRT; 203 AA.
AC P36978;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptosomal-associated protein 25B (SNAP-25B).
GN Name=SNAP-B;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=94068448; PubMed=8248151;
RA Rieger C., Larhammar D.;
RT Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC -!- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of the nerve terminal.
CC -!- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, and piriform cortex, anterior thalamic nuclei, pontine nuclei, and granule cells of the cerebellum.
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

EMBL; L22976; AAA16538.1; -; mRNA.
DR PIR; I50481; I50481.
DR HSP; P13795; 1SFC.
DR SMR; P36978; 7-82, 128-201.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; t-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; t-SNARE; 2.
KW Coiled coil; Glycoprotein; Multigene family; Repeat; Synaptosome.
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 137 199 t-SNARE coiled-coil homology 2.
FT CDS 137 199 Cys-rich.
FT COMPIAS 85 92 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 77 77 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 185 185 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 203 AA; 22664 MW; 8DFBEBDBE37D6D7 CRC64;

Query Match 100.0%; Score 68; DB 1; Length 203;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANORATKML 15
Db 187 TRIDEANORATKML 200

RESULT 6
O93579 BRARE PRELIMINARY; PRT; 203 AA.
AC O93579;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein 25.2.
GN Name=snap25b; Synonym=Snap;
OS Brachydanio rerio (Zebrafish)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=99057281; PubMed=9843147;
RX DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNRL13.3.CO;2-Z;
RA Rieger C., Salanek E., Soderberg C., Gates M., Postlethwait J.H., Larhammar D.;
RT Cloning of two loci for synapse protein Snap25 in zebrafish: comparison of paralogous linkage groups suggests loss of one locus in the mammalian lineage.
RL J. Neurosci. Res. 54:563-573(1998).
DR EMBL; AF091594; AAC64290.1; -; mRNA.
DR HSP; P60881; 1JTH.
DR SMR; O93579; 7-82, 128-201.
DR ZFIN; ZDB-GENE-980526-392; snap25b.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; t-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; t-SNARE; 2.
KW Synaptosome.
SQ SEQUENCE 203 AA; 22647 MW; 93B7590DD0C93F38 CRC64;

Query Match 100.0%; Score 68; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANORATKML 15
Db 187 TRIDEANORATKML 200

RESULT 7
O6PC54 BRARE PRELIMINARY; PRT; 203 AA.
AC O6PC54;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Synaptosome-associated protein 25 b.
GN Name=snap25b;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wild-Eye; TISSUE=EYE;
RX MEDLINE=23386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bernaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards D., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences,"
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wild-type; TISSUE=B-eye;
RA Strauberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059469; AAH59469.1; -; mRNA.
DR ZFIN; O6PC54; 7-82, 128-201.
DR ZFIN; ZDB-GENE-980526-392; snap25b.
DR GO; GO:0019171; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; T-SNARE; 2.
KW Synaptosome.
SQ SEQUENCE 203 AA; 22693 MW; 48D759DD0C1179A CRC64;

Query Match 100.0%; Score 68; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKML 15
|||||
Db 187 TRIDEANORATKML 200

RESULT 8
SN25A_CARAU STANDARD; PRT; 204 AA.
ID SN25A_CARAU
AC P36977;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptosomal-associated protein 25A (SNAP-25A).
OS Name=SNAP-A;
GN Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RX MEDLINE=94068448; PubMed=8248151;
RA Risinger C., Latham D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid
RT goldfish,"
RT Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC -1- FUNCTION: May play an important role in the synaptic function of
CC specific neuronal systems. Associates with proteins involved in
CC vesicle docking and membrane fusion.
CC -1- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
CC the nerve terminal.
CC -1- SIMILARITY: Belongs to the SNAP-25 family.
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; L22973; AAA16537.1; -; mRNA.
DR PIR; I50480; I50480.
DR HSP; P33795; IN78.
DR SNR; P36977; 7-83, 129-202.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; T-SNARE; 2.
KW Coiled coil; Multigene family; Repeat; Synaptosome.
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 138 200 t-SNARE coiled-coil homology 2.
FT COMPIAS 85 92 Cys-rich
SQ SEQUENCE 204 AA; 22843 MW; 458BBECFCFC09189 CRC64;
Query Match 100.0%; Score 68; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKML 15
|||||
Db 188 TRIDEANORATKML 201

RESULT 9
Q705J6_LATJA PRELIMINARY; PRT; 204 AA.
ID Q705J6_LATJA
AC Q705J6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Synaptosomal-associated protein 25.
GN Name=snap-25;
OS Lateolabrax japonicus (Japanese sea perch) (Japanese sea bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Moronidae; Lateolabrax.
OX NCBI_TaxID=8164;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Chen K., Huang X.H.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ619993; CAF04071.1; -; mRNA.
DR SNR; Q705J6; 7-83, 129-202.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; T-SNARE; 2.
SQ SEQUENCE 204 AA; 22842 MW; 8F77B18D591509B2 CRC64;
Query Match 100.0%; Score 68; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKML 15
|||||
Db 188 TRIDEANORATKML 201

```

RESULT 10
Q5TZ66_BRARE
ID Q5TZ66_BRARE PRELIMINARY; PRT; 204 AA.
AC Q5TZ66;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Synaptosomal-associated protein (SNAP).
GN Name=snap25a; Synonyms=OTDARP0000005563; ORFNames=DKEYP-8F4.6-001;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1]
RN NUCLEOTIDE SEQUENCE.
RA Lovell J.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RA Donaldson S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX465184; CAI21360.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69031.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69031.1; JOINED; Genomic DNA.
DR EMBL; BX465184; CAI21359.1; JOINED; Genomic DNA.
DR SMR; Q5TZ66; 7-83, 129-202.
DR Ensembl; ENSDARG00000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
KW Synaptosome.
SQ SEQUENCE 204 AA; 22857 MW; B53CF5F3D1C69EA5 CRC64;

Query Match 100.0%; Score 68; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANORATKML 15
Db 188 TRIDEANORATKML 201

RESULT 11
Q5TZ65_BRARE
ID Q5TZ65_BRARE PRELIMINARY; PRT; 204 AA.
AC Q5TZ65;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Synaptosomal-associated protein (SNAP).
GN Name=snap25a; Synonyms=OTDARP0000005690; ORFNames=DKEYP-8F4.6-002;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1]
RN NUCLEOTIDE SEQUENCE.
RA Lovell J.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RA Donaldson S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX465184; CAH69032.1; -; Genomic DNA.
DR EMBL; BX470246; CAI21360.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69032.1; JOINED; Genomic DNA.

```

```

DR EMBL; BX465184; CAI21360.1; JOINED; Genomic_DNA.
DR SMR; Q5TZ65; 7-83, 129-202.
DR Ensembl; ENSDARG00000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR SMART; SM00397; t_SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
KW Synaptosome.
SQ SEQUENCE 204 AA; 22878 MW; FBC79AB7015AC0ED CRC64;

Query Match 100.0%; Score 68; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANORATKML 15
Db 188 TRIDEANORATKML 201

RESULT 12
SNP25_CHICK
ID SNP25_CHICK STANDARD; PRT; 206 AA.
AC P60878; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
DE 25 kDa protein) (Super protein) (SUP).
GN Name=SNAP25; Synonyms=SNAP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RN NUCLEOTIDE SEQUENCE (ISOFORM SNAP25B).
RP STRAIN=White leghorn; TISSUE=Retina;
MEDLINE=91126080; PubMed=1992470;
RA Catsicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,
RA Wilson M.C.;
RT "Expression of a conserved cell-type-specific protein in nerve
RT terminals coincides with synaptogenesis.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
[2]
RN NUCLEOTIDE SEQUENCE (ISOFORMS SNAP25A AND SNAP25B).
RX MEDLINE=93389738; PubMed=8377193;
RA Bark I.C.;
RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon
RT encoding distinct isoforms of the protein.";
RL J. Mol. Biol. 233:67-76(1993).
CC -!- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion (By
CC similarity).
CC -!- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1
CC and SNAP25BP. Binds STXBp6. Found in a ternary complex with STX1A
CC and VAMP8 (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60878-1, P13795-1;
CC Sequence=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60878-2, P13795-2;

```


RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 11-81 AND 141-202 IN COMPLEX
RP WITH STX1A; CPLX1 AND VAMP2, AND NMR ANALYSIS.
RP MEDLINE=21822661; PubMed=11832227; DOI=10.1016/S0896-6273(02)00583-4;
RX Chen X., Tomchick D.R., Kovrigin E., Arac D., Machius M.,
RX Suedhof T.C., Rizo J.;
RA "Three-dimensional structural structure of the complexin/SNARE complex.";
RL Neuron 33:397-409(2002).
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion.
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
CC SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with
CC STX1A and VAMP8 (By similarity).
CC -1- INTERACTION:
CC Q8IUH5:HIP14; NDExp=1; IntAct=EBI-524785, EBI-524753;
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment-Isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60880-1, P13795-1;
CC Sequence=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60880-2, P13795-2;
CC Sequence=VSP_006186;
CC -1- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, and
CC piriform cortex, anterior thalamic nuclei, pontine nuclei, and
CC granule cells of the cerebellum.
CC -1- PTM: Palmitoylated (By similarity).
CC -1- SIMILARITY: Belongs to the SNAP-25 family.
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; L19760; AAC37545.1; -; mRNA.
CC EMBL; L19761; AAC37546.1; -; mRNA.
CC EMBL; D21467; BAA22370.1; -; mRNA.
CC EMBL; AL023913; CAC34534.1; -; Genomic DNA.
CC EMBL; AL023913; CAC34535.1; -; Genomic DNA.
CC EMBL; AL023913; CAD56158.1; -; Genomic DNA.
CC EMBL; AL023913; CAB42860.1; -; Genomic DNA.
CC EMBL; BC010647; AAH10647.1; -; mRNA.
CC F01; I53735; I53735.
CC F01; I67823; I67823.
CC PDB; 1XIL; X-ray; C=11-80, D=141-203.
CC PDB; 1XIG; X-ray; B=146-204.
CC SMR; P60880; 7-83, 131-204.
CC IntAct; P60880;
CC Ensembl; ENSG00000132639; Homo sapiens.
CC HGNC; HGNC:11132; SNAP25.
CC H-InvDB; HIX0015639; -;
CC MIM; 600322; -;
CC GO; GO:0007269; P:neurotransmitter secretion; NAS.
CC GO; GO:0001504; P:neurotransmitter uptake; NAS.
CC GO; GO:0050796; P:regulation of insulin secretion; TAS.
CC GO; GO:0007268; P:synaptic transmission; NAS.
CC GO; GO:0016081; P:synaptic vesicle docking during exocytosis; NAS.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T_SNARE.

DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS0192; t-SNARE; 2.
KW 3D-structure; Alternative splicing; Coiled coil; Lipoprotein;
KW Palmitate; Phosphorylation; Repeat; Synaptosome.
FT DOMAIN 19 81
FT t-SNARE coiled-coil homology 1.
FT t-SNARE coiled-coil homology 2.
FT Cys-rich.
FT COMPBIAS 85 92
FT SITE 180 181
FT MOD_RES 138 138
FT MOD_RES 187 187
FT VARSPIC 58 89
FT
FT HELIX 7 82
FT HELIX 142 201
FT TURN 202 202
SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
Query Match 100.0%; Score 68; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TRIDEANORATKML 15
DB 190 TRIDEANORATKML 203
RESULT 14
SNP25 MACMU
ID SNP25 MACMU STANDARD; PRT; 206 AA.
AC P60877; P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
DE 25 kDa protein).
GN Name=SNAP25;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hippocampus;
RA Jensen M.J., Smith L.A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion (By
CC similarity).
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
CC SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with
CC STX1A and VAMP8 (By similarity).
CC -1- SIMILARITY: Belongs to the SNAP-25 family.
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AF240770; AAP64477.1; -; mRNA.
CC SMR; P60877; 7-83, 131-204.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T_SNARE.

CC -i- PTM: Palmitoylated (By similarity).
 CC -i- SIMILARITY: Belongs to the SNAP-25 family.
 CC -i- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; M22012; AAA61741.1; -; mRNA.
 CC EMBL; AF483516; AAL90790.1; -; mRNA.
 CC EMBL; AF483517; AAL90791.1; -; mRNA.
 CC EMBL; AK078038; BAC37105.1; -; mRNA.
 CC EMBL; BC018249; AAH18249.1; -; mRNA.
 CC EMBL; BC018249; AAH18249.1; -; mRNA.
 CC PIR; A33623; A33623.
 CC PDB; 2BU0; Model; C=18-82, D=139-206.
 CC SMR; P60879; 7-83, 131-204.
 CC Ensembl; ENSMUSG0000027273; Mus musculus.
 CC MGI; MGI:98331; Snap25.
 CC GO; GO:0005886; C:plasma membrane; TAS.
 CC GO; GO:0000149; F:SNARE binding; IDA.
 CC GO; GO:0007269; P:neurotransmitter secretion; IMP.
 CC InterPro; IPR000928; SNAP-25.
 CC InterPro; IPR000727; T-SNARE.
 CC Pfam; PF00835; SNAP_25; 1.
 CC Pfam; PF05739; SNARE; 1.
 CC SMART; SM00397; t-SNARE; 2.
 CC PROSITE; PS50192; T-SNARE; 2.
 CC 3D-structure; Alternative splicing; Coiled coil; Lipoprotein;
 CC Palmitate; Phosphorylation; Repeat; Synaptosome.
 CC FT DOMAIN 19 81
 FT DOMAIN 140 202
 FT COMPBIAS 85 92
 FT SITE 180 181
 FT MOD_RES 138 138
 FT MOD_RES 187 187
 FT VARSPIC 58 89
 FT ERIEGMDQINKMKEAKENLTLGKFCGLCV -> DRVVEE
 FT GNNHINQDMKEAKENLKDGLKCCGLFI (in isoform
 FT SNAP-25a).
 FT /FTId=VSP_010019.
 SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;

Query Match 100.0%; Score 68; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred.No. 0.00068;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 TRIDEANORATKML 15
 |||||
 Db 190 TRIDEANORATKML 203

Search completed: April 3, 2006, 15:46:25
 Job time : 82.4954 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:30:10 ; Search time 8.66055 Seconds
(without alignments)
177.756 Million cell updates/sec

Title: US-09-942-098-91
Perfect score: 68
Sequence: 1 XTRIDEANQRATKMLX 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Pir1.*
- 2: Pir2.*
- 3: Pir3.*
- 4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	203	2 I50481	synapse protein SN
2	68	100.0	204	2 I50480	synapse protein SN
3	68	100.0	206	2 A37861	synaptosomal-assoc
4	68	100.0	206	2 I53735	nerve terminal pro
5	68	100.0	206	2 I67823	nerve terminal pro
6	68	100.0	206	2 A33623	synaptosomal-assoc
7	54	79.4	210	2 I50552	synapse protein -
8	42	61.8	83	2 A33854	outer membrane lip
9	41	60.3	2288	2 T29999	hypothetical prote
10	40	58.8	540	2 T34187	hypothetical prote
11	38	55.9	151	2 G95369	SVB2 transcriptio
12	38	55.9	158	2 J65297	vesicle-membrane f
13	38	55.9	176	2 J65297	hypothetical prote
14	38	55.9	210	2 J65512	SNARE protein 23 -
15	38	55.9	211	2 J65296	vesicle-membrane f
16	38	55.9	317	2 A72295	conserved hypothet
17	38	55.9	494	2 S64386	pre-mRNA splicing
18	38	55.9	1578	2 S76238	hypothetical prote
19	37	54.4	241	1 RRNZPP	phosphoprotein p -
20	37	54.4	241	1 RRNZPP	phosphoprotein p -
21	37	54.4	885	2 S59660	anaphase spindle e
22	37	54.4	6669	2 S55024	nebulin, skeletal
23	36	52.9	129	2 C84375	hypothetical prote
24	36	52.9	393	2 T32127	hypothetical prote
25	36	52.9	401	2 E81436	transmembrane tran
26	36	52.9	642	2 G90551	lipoprotein (impor
27	36	52.9	660	2 F98020	hypothetical prote
28	36	52.9	680	2 H70347	outer membrane pro
29	36	52.9	686	1 E71106	probable DNA topoi

30	36	52.9	1056	2 T33167	hypothetical prote
31	36	52.9	1361	2 A29959	DNA-directed RNA p
32	35	51.5	71	2 D84748	hypothetical prote
33	35	51.5	181	2 A45422	ADP-ribosylation f
34	35	51.5	181	2 JC4946	ADP-ribosylation f
35	35	51.5	227	2 D83271	probable ATP-bindi
36	35	51.5	263	2 A86272	protein FL6A14.10
37	35	51.5	313	2 T15167	hypothetical prote
38	35	51.5	331	2 T05428	hypothetical prote
39	35	51.5	365	2 B70435	hypothetical prote
40	35	51.5	365	2 D97848	hypothetical prote
41	35	51.5	408	2 AD2473	hypothetical prote
42	35	51.5	417	2 S73223	MG288 homolog G07
43	35	51.5	425	2 D84888	hypothetical prote
44	35	51.5	448	2 G69960	exodeoxyribonuclea
45	35	51.5	477	2 F83519	conserved hypothet

ALIGNMENTS

RESULT 1

I50481
synapse protein SNAP-25 - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50481
R;Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Accession: I50481
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-203 <RIS>
A;Cross-references: UNIPROT:P36978; UNIPARC:UPI0000135B03; GB:L22976; NID:G349430; PIDN:?
C;Genetics:
A;Gene: SNAP-25

Query Match 100.0%; Score 68; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15

Db 187 TRIDEANQRATKML 200
|||||
|||||

RESULT 2

I50480
synapse protein SNAP-25 - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50480
R;Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Accession: I50480
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-204 <RIS>
A;Cross-references: UNIPROT:P36977; UNIPARC:UPI0000135B02; GB:L22973; NID:G349426; PIDN:?
C;Genetics:
A;Gene: SNAP-25

Query Match 100.0%; Score 68; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15

Db 188 TRIDEANQRATKML 201
|||||
|||||

RESULT 3

A37861
synaptosomal-associated 25K protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
C;Accession: A37861
R;Catsicas, S.; Iarhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coincides with the expression of synaptophysin in the same nerve terminals
A;Reference number: A37861; MUID:91126080; PMID:1992470
A;Accession: A37861
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <CAT>
A;Cross-references: UNIPROT:P60878; UNIPARC:UPI0000001103; GB:M57957; NID:g212673; PIDN:

Query Match 100.0%; Score 68; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANORATKML 15
|||||
Db 190 TRIDEANORATKML 203

RESULT 4

I53735
nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I53735
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A;Reference number: I53735; MUID:94156217; PMID:8112622
A;Accession: I53735
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: UNIPROT:P60880; UNIPARC:UPI000002B3DD; GB:L19760; NID:g307425; PIDN:
C;Genetics:
A;Gene: GDB:SNAP
A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 68; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANORATKML 15
|||||
Db 190 TRIDEANORATKML 203

RESULT 5

I67823
nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I67823
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A;Reference number: I53735; MUID:94156217; PMID:8112622
A;Accession: I67823
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: UNIPROT:P60880; UNIPARC:UPI0000001103; GB:L19761; NID:g307427; PIDN:
C;Genetics:
A;Gene: GDB:SNAP

A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 68; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANORATKML 15
|||||
Db 190 TRIDEANORATKML 203

RESULT 6

A33623
synaptosomal-associated 25K protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 09-Jul-2004
C;Accession: A33623
R;Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.; v
J. Cell Biol. 109, 3039-3052, 1989
A;Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differer
A;Reference number: A33623; MUID:90078337; PMID:2592413
A;Accession: A33623
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <OYL>
A;Cross-references: UNIPROT:P60879; UNIPARC:UPI0000001103; GB:M22012; GB:X51673; NID:g20(

Query Match 100.0%; Score 68; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANORATKML 15
|||||
Db 190 TRIDEANORATKML 203

RESULT 7

I50552
synapse protein - marbled electric ray
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50552
R;Risiger, C.; Blomqvist, A.G.; Lundell, I.; Lambertsson, A.; Nassel, D.; Pieribone, V.;
J. Biol. Chem. 268, 24408-24414, 1993
A;Title: Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25) shc
A;Reference number: A49513; MUID:94043281; PMID:8226991
A;Accession: I50552
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-210 <RIS>
A;Cross-references: UNIPROT:P36976; UNIPARC:UPI0000135AFB; GB:L22020; NID:g431296; PIDN:

Query Match 79.4%; Score 54; DB 2; Length 210;
Best Local Similarity 84.6%; Pred. No. 0.02;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RIDEANORATKML 15
|||||
Db 198 RIDEANORATKML 210

RESULT 8

A33854
outer membrane lipoprotein I precursor - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 09-Jul-2004
C;Accession: A33854; S04834; A44834; A83288
R;Duchene, M.; Barron, C.; Schweizer, A.; von Specht, B.U.; Domdey, H.
J. Bacteriol. 171, 4130-4137, 1989
A;Title: Pseudomonas aeruginosa outer membrane lipoprotein I gene: molecular cloning, seq
A;Reference number: A33854; MUID:89327122; PMID:2502533
A;Accession: A33854

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <DUC>
A;Cross-references: UNIPROT:P11221; UNIPARC:UPI000002C273; GB:M25761; NID:G151334; PIDN:R;Cornellis, P.; Bouia, A.; Belarbi, A.; Guyonvarch, A.; Kammerer, B.; Hannaert, V.; Hube Mol. Microbiol. 3, 421-428, 1989
A;Title: Cloning and analysis of the gene for the major outer membrane lipoprotein from A;Reference number: S04834; MUID:89313294; PMID:2473376
A;Accession: S04834
A;Molecule type: DNA
A;Residues: 1-83 <COR>
A;Cross-references: UNIPARC:UPI000002C273; EMBL:X13748; NID:G45344; PIDN:CAA32013.1; PIDN:CAA32013.1; PIDN:CAA32013.1; PIDN:CAA32013.1
A;Note: The authors translated the codon GAA for residue 78 as Gly
R;Saint-Onge, A.; Romeyer, F.; Lebel, P.; Masson, L.; Brousseau, R.
J. Gen. Microbiol. 138, 733-741, 1992
A;Title: Specificity of the Pseudomonas aeruginosa PAO1 lipoprotein I gene as a DNA probe A;Reference number: A44834; MUID:92268853; PMID:1588307
A;Accession: A44834
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <SAI>
A;Cross-references: UNIPARC:UPI000002C273; GB:X58714; GB:S36066; NID:G433509; PIDN:CAA41
A;Experimental source: PAO1
A;Note: sequence extracted from NCBI backbone (NCBIN:103666, NCBIP:103667)
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; B. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, L.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83288
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <STO>
A;Cross-references: UNIPARC:UPI000002C273; GB:AE004712; GB:AE004091; NID:G9948940; PIDN: A;Experimental source: strain PAO1
C;Genetics:
A;Gene: oprI; PA2953
A;Keywords: lipid binding; lipoprotein; membrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
P;20-83/Product: lipoprotein I #status predicted <MAT>
Query Match 61.8%; Score 42; DB 2; Length 83;
Best Local Similarity 72.7%; Pred. No. 1.2; Indels 1; Gaps 0;
Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 0;
Qy 5 DEANORATKML 15
Db 67 DEANERLRML 77
RESULT 9
T29999
hypothetical protein ZC8.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29999
R;Latreille, P.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid ZC8.
A;Reference number: T20719
A;Accession: T29999
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-2288 <LAT>
A;Cross-references: UNIPROT:Q23081; UNIPARC:UPI000017BCE7; EMBL:U64862; PIDN:AA52624.1; A;Experimental source: strain Bristol N2; clone ZC8
C;Genetics:
A;Gene: CBSP:ZC8.4
A;Map position: X
A;Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 1686/
Query Match 60.3%; Score 41; DB 2; Length 2288;

Best Local Similarity 57.1%; Pred. No. 63; Indels 4; Gaps 0;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 2 TRIDEANORATKML 15
Db 627 TRIDELNRRVENLL 640
RESULT 10
T34187
hypothetical protein C49H3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 12-Jul-2004
C;Accession: T34187
R;Wu, X.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid C49H3.
A;Reference number: Z21485
A;Accession: T34187
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-540 <WUX>
A;Cross-references: UNIPROT:Q9GYQ4; UNIPARC:UPI000017CE0F; EMBL:U42436; PIDN:AAA83492.1; C;Genetics:
A;Gene: CBSP:C49H3.1
A;Introns: 247/2; 319/2; 393/3
Query Match 58.8%; Score 40; DB 2; Length 540;
Best Local Similarity 59.3%; Pred. No. 21; Indels 1; Gaps 0;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 4 IDEANORATKML 15
Db 277 LEEANQRADRL 288
RESULT 11
G95369
SyrB2 transcription regulator [imported] - Sinorhizobium meliloti (strain 1021) magaplas C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: G95369
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowes : Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: G95369
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <KUR>
A;Cross-references: UNIPROT:Q9Z3Q1; UNIPARC:UPI0000136338; GB:AE006469; PIDN:AAK65521.1; A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Komp, C.; Lelaure, habault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: syrB2
A;Genome: plasmid
Query Match 55.9%; Score 38; DB 2; Length 151;
Best Local Similarity 53.8%; Pred. No. 13; Indels 3; Gaps 0;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 3 RIDEANORATKML 15
Db 121 RLEENQRLKLL 133

RESULT 12
JC5297
vesicle-membrane fusion protein SNAP-23B - human
C;Species: Homo sapiens (man)
C;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: JC5297
R;Mollinedo, F.; Lazo, P.A.
Biochem. Biophys. Res. Commun. 231, 808-812, 1997
A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23 in human neutrophils
A;Reference number: JC5296; MUID: 97224437; PMID: 9070898
A;Accession: JC5297
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-158 <MOL>
A;Cross-references: UNIPROT:O00161; UNIPARC:UPI000002B3DC; GB:Y09568; NID:g1924943; PIDN: 15
A;Experimental source: neutrophils
C;Comment: This protein is involved in regulating exocytosis in human neutrophils, a central role in the insulin-induced translocation of vesicles containing insulin.

Query Match 55.9%; Score 38; DB 2; Length 158;
Best Local Similarity 61.5%; Pred. No. 13; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 RIDEANORATKML 15
||| ||| ||| :
Db 144 RIDIANARAKKLI 156

RESULT 13
D72668
hypothetical protein APE0770 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D72668
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahashi, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kato, M.
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
A;Reference number: A72450; MUID: 99310339; PMID: 10382966
A;Accession: D72668
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-176 <KAW>
A;Cross-references: UNIPROT:Q9YDZ9; UNIPARC:UPI000005DCA1; DDBJ:AP0000060; NID:g5104188;
C;Genetics:
A;Experimental source: strain K1
C;Gene: APE0770
C;Superfamily: Aeropyrum pernix hypothetical protein APE0770

Query Match 55.9%; Score 38; DB 2; Length 176;
Best Local Similarity 46.2%; Pred. No. 15; Mismatches 5; Indels 0; Gaps 0;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 RIDEANORATKML 15
: ||| ||| ||| :
Db 126 QVNDNDNORSTRLL 138

RESULT 14
JC5512
SNARE protein 23 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5512
R;Araki, S.; Tamori, Y.; Kawanishi, M.; Shinoda, H.; Masugi, J.; Mori, H.; Niki, T.; Okabe, K.
Biochem. Biophys. Res. Commun. 234, 257-262, 1997
A;Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c.
A;Reference number: JC5512; MUID: 97312558; PMID: 9168999
A;Accession: JC5512
A;Molecule type: mRNA
A;Residues: 1-210 <ARA>
A;Cross-references: UNIPROT:O09044; UNIPARC:UPI000002B5C; DDBJ:AB000822; NID:g2189950;

C;Comment: This protein is involved in the insulin-induced translocation of vesicles containing insulin.

Query Match 55.9%; Score 38; DB 2; Length 210;
Best Local Similarity 61.5%; Pred. No. 18; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 RIDEANORATKML 15
||| ||| ||| :
Db 196 RIDIANTRAKKLI 208

RESULT 15
JC5296
vesicle-membrane fusion protein SNAP-23A - human
C;Species: Homo sapiens (man)
C;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: JC5296
R;Mollinedo, F.; Lazo, P.A.
Biochem. Biophys. Res. Commun. 231, 808-812, 1997
A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23 in human neutrophils
A;Reference number: JC5296; MUID: 97224437; PMID: 9070898
A;Accession: JC5296
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-211 <MOL>
A;Cross-references: UNIPROT:O00161; UNIPARC:UPI0000000A2C; GB:Y09567; NID:g1924941; PIDN: 15
C;Comment: This protein is involved in regulating exocytosis in human neutrophils, a central role in the insulin-induced translocation of vesicles containing insulin.

Query Match 55.9%; Score 38; DB 2; Length 211;
Best Local Similarity 61.5%; Pred. No. 18; Mismatches 2; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 RIDEANORATKML 15
||| ||| ||| :
Db 197 RIDIANARAKKLI 209

Search completed: April 3, 2006, 15:31:24
Job time : 9.66055 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model
Run on: April 3, 2006, 15:27:08 ; Search time 82.055 Seconds
(without alignments)
85.675 Million cell updates/sec

Title: US-09-942-098-91

Perfect score: 68

Sequence: 1 XTRIDEANQRATKMLX 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A Geneseq 21:*
- 1: geneseqp1980s:*
 - 2: geneseqp1990s:*
 - 3: geneseqp2000s:*
 - 4: geneseqp2001s:*
 - 5: geneseqp2002s:*
 - 6: geneseqp2003as:*
 - 7: geneseqp2003bs:*
 - 8: geneseqp2004s:*
 - 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	16	AAE36736	Aae36736 Fret subs
2	68	100.0	16	AAE36739	Aae36739 Fret subs
3	68	100.0	16	ABW01795	Abw01795 FRET subs
4	68	100.0	16	ABW01792	Abw01792 FRET subs
5	68	100.0	17	AAY44057	Aay44057 Human SNA
6	68	100.0	17	AAY44021	Aay44021 Amino aci
7	68	100.0	17	ASG69065	Asg69065 Human pol
8	68	100.0	17	AAE36675	Aae36675 Human SNA
9	68	100.0	17	ABW01731	Abw01731 Human SNA
10	68	100.0	17	ADM97046	Adm97046 Botulinum
11	68	100.0	17	ADM97062	Adm97062 Botulinum
12	68	100.0	17	AEA14920	Aea14920 Human SNA
13	68	100.0	18	AAE36677	Aae36677 Human SNA
14	68	100.0	18	ABW01733	Abw01733 Botulinum
15	68	100.0	18	ADM97048	Adm97048 Human SNA
16	68	100.0	18	AEA14922	Aea14922 Human SNA
17	68	100.0	19	AAE36730	Aae36730 Fret subs
18	68	100.0	19	AAE36740	Aae36740 Fret subs
19	68	100.0	19	AAE36737	Aae36737 Fret subs
20	68	100.0	19	ABW01793	Abw01793 FRET subs
21	68	100.0	19	ABW01796	Abw01796 FRET subs
22	68	100.0	19	ABW01786	Abw01786 FRET subs
23	68	100.0	19	ABW01786	Abw01786 FRET subs
24	68	100.0	19	ADP13171	Adp13171 SNAP 25 p

25	68	100.0	20	AAW30100	Aaw30100 Neurotran
26	68	100.0	20	ABW01798	Abw01798 FRET subs
27	68	100.0	21	AAE36734	Aae36734 FRET subs
28	68	100.0	21	ABW01790	Abw01790 FRET subs
29	68	100.0	22	AAE36738	Aae36738 FRET subs
30	68	100.0	22	ABW01794	Abw01794 FRET subs
31	68	100.0	23	AAE36733	Aae36733 FRET subs
32	68	100.0	23	ABW01789	Abw01789 FRET subs
33	68	100.0	24	AAE36735	Aae36735 FRET subs
34	68	100.0	24	ABW01791	Abw01791 FRET subs
35	68	100.0	26	AAW30099	Aaw30099 Neurotran
36	68	100.0	33	AAE36682	Aae36682 Goldfish
37	68	100.0	33	AAE36683	Aae36683 Goldfish
38	68	100.0	33	AAE36678	Aae36678 SNAP-25 p
39	68	100.0	33	ABW01739	Abw01739 Goldfish
40	68	100.0	33	ABW01734	Abw01734 Mouse SNA
41	68	100.0	33	ABW01738	Abw01738 Goldfish
42	68	100.0	33	ADM97054	Adm97054 Botulinum
43	68	100.0	33	ADM97053	Adm97053 Botulinum
44	68	100.0	33	ADM97049	Adm97049 Botulinum
45	68	100.0	33	AEA14927	Aea14927 Goldfish

ALIGNMENTS

RESULT 1

AAE36736
ID AAE36736 standard; peptide; 16 AA.

XX AC AAE36736;

XX 07-AUG-2003 (first entry)

XX Fret substrate peptide #7 used in the invention.

XX Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
KW cosmetic.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Modified-site 1
FT /note= "Fluorescein-modified lysine; This residue is
FT given as Xaa in the sequence shown as SEQ ID NO: 91 in
FT the sequence listing of the specification"

FT Modified-site 16
FT /note= "Tetramethylrhodamine-modified lysine; C-terminal
FT amide; This residue is given as Xaa in the sequence shown
FT as SEQ ID NO: 91 in the sequence listing of the
FT specification"

XX WO2003020948-A2.

XX 13-MAR-2003.

XX 22-AUG-2002; 2002WO-US027145.

XX 28-AUG-2001; 2001US-00942024.

XX (ALLR) ALLERGAN INC.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-290198/28.

XX Botulinum serotype A/E substrate useful for assaying protease activity of
PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
PT toxin recognition sequence that includes a cleavage site.

XX Example 1; Page 115; 168pp; English.

CC The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is fret
 CC substrate peptide used in the exemplification of the invention
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 68; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.1e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
 |||||
 Db 2 TRIDEANQRATKML 15

RESULT 2
 AAE36739
 ID AAE36739 standard; peptide; 16 AA.

AC AAE36739;

XX 07-AUG-2003 (first entry)

DT Fret substrate peptide #10 used in the invention.

DE Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;

KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;

KW cosmetic.

XX Unidentified.

OS Key Location/Qualifiers

FH Modified-site 1 /note= "DABCYL-modified Lysine; This residue is given as
 FT Xaa in the sequence shown as SEQ ID NO: 94 in the

FT sequence listing of the specification"

FT Modified-site 16 /note= "EDANS-modified Glutamate; C-terminal amide; This
 FT residue is given as Xaa in the sequence shown as SEQ ID
 FT NO: 94 in the sequence listing of the specification"

XX WO2003020948-A2.

PN 13-MAR-2003.

XX 22-AUG-2002; 2002WO-US027145.

XX 28-AUG-2001; 2001US-00942024.

XX (ALLR) ALLERGAN INC.

PA Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-290198/28.

XX Botulinum serotype A/E substrate useful for assaying protease activity of

PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 XX toxin recognition sequence that includes a cleavage site.
 PS Example 1; Page 115; 168pp; English.

XX The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is fret
 CC substrate peptide used in the exemplification of the invention
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 68; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.1e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
 |||||
 Db 2 TRIDEANQRATKML 15

RESULT 3

ABW01795
 ID ABW01795 standard; peptide; 16 AA.

AC ABW01795;

XX 12-FEB-2004 (first entry)

DT FRET substrate #8 to analyse proteolytic activity of botulinum toxin.

DE Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;

KW FRET; fluorescence resonance energy transfer.

XX Unidentified.

OS Key Location/Qualifiers

FH Modified-site 1 /note= "DABCYL labelled lysine"

FT Modified-site 16 /note= "EDANS labelled glutamate; C-terminal amide"

FT US2003143651-A1.

XX 31-JUL-2003.

XX 28-AUG-2001; 2001US-00942098.

XX 28-AUG-2001; 2001US-00942098.

XX (STEW/) STEWARD L E.

PA (FERN/) FERNANDEZ-SALAS E.

PA (AOKI/) AOKI K R.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-829791/77.

XX Determining clostridial toxin protease activity, by treating sample with
 PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
 PT sequence, under conditions which exhibit resonance energy transfer.

XX Example 1; Page 29; Opp; English.

XX The present invention provides clostridial toxin substrates useful in
 CC assaying for the protease activity of any clostridial toxin including
 CC toxins of all serotypes as well as tetanus toxins. The present sequence
 CC is FRET (fluorescence resonance energy transfer) substrate to analyse
 CC proteolytic activity of botulinum toxin. This substrate is used in the
 CC exemplification of the invention

XX Sequence 16 AA;

Query Match 100.0%; Score 68; DB 7; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.1e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15
 |||||
 Db 2 TRIDEANQRATKML 15

RESULT 4

ABW01792
 ID ABW01792 standard; peptide; 16 AA.

AC ABW01792;

XX 12-FEB-2004 (first entry)

XX FRET substrate #5 to analyse proteolytic activity of botulinum toxin.

XX Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;

KW FRET; fluorescence resonance energy transfer.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Fluoresceinated lysine"

FT Modified-site 16 /note= "Tetramethylrhodamine labelled lysine; C-terminal amide"

FT FT
 FT FT
 FT FT

XX US2003143651-A1.

XX 31-JUL-2003.

XX 28-AUG-2001; 2001US-00942098.

XX 28-AUG-2001; 2001US-00942098.

XX (STEW/) STEWARD L E.

PA (FERN/) FERNANDEZ-SALAS E.

PA (AOKI/) AOKI K R.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-829791/77.

XX Determining clostridial toxin protease activity, by treating sample with
 PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
 PT sequence, under conditions which exhibit resonance energy transfer.

XX Example 1; Page 29; Opp; English.

XX The present invention provides clostridial toxin substrates useful in
 CC assaying for the protease activity of any clostridial toxin including
 CC toxins of all serotypes as well as tetanus toxins. The present sequence
 CC is FRET (fluorescence resonance energy transfer) substrate to analyse

CC proteolytic activity of botulinum toxin. This substrate is used in the
 CC exemplification of the invention

SQ Sequence 16 AA;

Query Match 100.0%; Score 68; DB 7; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.1e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15

Db 2 TRIDEANQRATKML 15

RESULT 5

AAY44057

ID AAY44057 standard; peptide; 17 AA.

XX AAY44057;

XX 18-JAN-2000 (first entry)

XX Human SNAP25 (amino acids 187-203) analogue #36.

XX Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;
 KW fluorescamine; detection; human; synaptosomal protein; SNAP25;
 KW hydrolysis; amino group.

XX Homo sapiens.

OS Synthetic.

XX US5965699-A.

XX 12-OCT-1999.

XX 06-NOV-1996; 96US-00743894.

XX 06-NOV-1996; 96US-00743894.

XX (USSA) US SEC OF ARMY.

XX Bostian KA, Schmidt JJ;

XX WPI; 1999-579939/49.

XX Quantitation of type A botulinum toxin.

XX Disclosure; Col 9; 28pp; English.

XX The invention relates to an enzymatic assay for the quantitation of type
 CC A botulinum toxin, by determining the proteolytic activity of botulinum
 CC neurotoxin type A using fluorescamine detection. Botulinum toxin A has
 CC been shown to cleave the synaptosomal neurotransmitter peptide SNAP25
 CC between residues 197-198. The method comprises adding an analogue (e.g.
 CC AAY44022-Y44076) of the SNAP25 peptide (AAY44021, amino acids 187-203 of
 CC human SNAP25) to a sample containing the botulinum toxin A so that
 CC hydrolysis of the peptide is initiated, then stopping hydrolysis of the
 CC peptide at different time points; and measuring the amount of hydrolysis
 CC at each time point by combining with a label capable of detecting free
 CC amino groups resulting from the hydrolysis. The amount of botulinum toxin
 CC A present in the sample is determined by comparing measurements with the
 CC amount of label produced from a known concentration of toxin measured
 CC under similar conditions. The method is useful for the quantitation of
 CC type A botulinum toxin

SQ Sequence 17 AA;

Query Match 100.0%; Score 68; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15

|||||

Db 4 TRIDEANORATKML 17

RESULT 6
 AAY44021
 ID AAY44021 standard; peptide; 17 AA.
 XX
 AC AAY44021;
 XX
 DT 18-JAN-2000 (first entry)
 XX
 DE Amino acids 187-203 of human SNAP25.
 XX
 KW Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;
 KW fluorescamine; detection; human; synaptosomal protein; SNAP25;
 KW hydrolysis; amino group.
 XX
 OS Homo sapiens.
 XX
 PN US5965699-A.
 XX
 PD 12-OCT-1999.
 XX
 PF 06-NOV-1996; 96US-00743894.
 XX
 PR 06-NOV-1996; 96US-00743894.
 XX
 PA (USSA) US SEC OF ARMY.
 XX
 PI Bostian KA, Schmidt JJ;
 XX
 DR WPI; 1999-579939/49.
 XX
 PT Quantitation of type A botulinum toxin.
 XX
 PS Claim 1; Col 4; 28pp; English.
 XX
 CC The invention relates to an enzymatic assay for the quantitation of type
 CC A botulinum toxin, by determining the proteolytic activity of botulinum
 CC neurotoxin type A using fluorescamine detection. The method comprises
 CC adding an analogue (e.g. AAY44022-Y44076) of this peptide (which
 CC represents amino acids 187-203 of the human synaptosomal protein SNAP25)
 CC to a sample containing the botulinum toxin A so that hydrolysis of the
 CC peptide is initiated, then stopping hydrolysis of the peptide at each
 CC different time points; and measuring the amount of hydrolysis at each
 CC time point by combining with a label capable of detecting free amino
 CC groups resulting from the hydrolysis. The amount of botulinum toxin A
 CC present in the sample is determined by comparing measurements with the
 CC amount of label produced from a known concentration of toxin measured
 CC under similar conditions. The method is useful for the quantitation of
 CC type A botulinum toxin
 XX

QY 2 TRIDEANORATKML 15
 DB 4 TRIDEANORATKML 17

Query Match 100.0%; Score 68; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 ABG69065
 ID ABG69065 standard; peptide; 17 AA.
 XX
 AC ABG69065;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Human polypeptide C-terminal fragment.
 XX

KW Botulinum neurotoxin light chain; BoNT LC; botulism; dystonia; pain;
 KW spasticity; ocular motility; facial dyskinesia; stiff-person syndrome;
 KW bladder dysfunction; segmental myoclonus; hyperkinetic disorder; human;
 KW cosmetic treatment; facial wrinkle; cerebral palsy; analgesic; relaxant;
 KW lower motor neuron hyperactivity; autonomic nerve function; muscular;
 KW immunostimulant; antibacterial.
 XX
 OS Homo sapiens.
 XX
 PN WO200236758-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 06-NOV-2001; 2001WO-US047230.
 XX
 PR 06-NOV-2000; 2000US-0246774P.
 PR 20-JUL-2001; 2001US-00910186.
 PR 09-AUG-2001; 2001US-0311966P.
 XX
 PA (USSA) US ARMY MEDICAL RES & MATERIAL COMMAND.
 XX
 PI Smith LA, Jensen M;
 XX
 DR WPI; 2002-575192/61.
 XX
 PT Novel nucleic acid molecule encoding botulinum neurotoxin light chain
 PT serotype A, useful for producing the neurotoxin for vaccination against
 PT botulism, comprises sequence expressible in host other than Clostridium.
 XX
 PS Example 25; Page 62; 166pp; English.
 XX
 CC The invention relates to a nucleic acid molecule encoding a botulinum
 CC neurotoxin light chain (BoNT LC) serotype A, where the DNA has a sequence
 CC that is expressible in a host organism other than Clostridium, or has a
 CC total A+T content that is less than about 70% The BoNT LC protein is
 CC useful in vaccination against botulism, for eliciting protective immunity
 CC in a mammal, for treating dystonias, spasticity, pain, ocular motility,
 CC facial dyskinesias, stiff-person syndrome, bladder dysfunction, segmental
 CC myoclonus, hyperkinetic disorders, cosmetic treatment of facial wrinkles,
 CC conditions characterised by hyperactivity of the lower motor neuron, and
 CC to control autonomic nerve function or tiptoe-walking due to stiff
 CC muscles common in children with cerebral palsy. The sequences are also
 CC useful for screening for botulinum neurotoxin inhibitors. This sequence
 CC represents a human polypeptide C-terminal fragment, used in the scope of
 CC the invention
 XX
 PS Sequence 17 AA;
 XX

Query Match 100.0%; Score 68; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKML 15
 DB 4 TRIDEANORATKML 17

Query Match 100.0%; Score 68; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 AAE36675
 ID AAE36675 standard; peptide; 17 AA.
 XX
 AC AAE36675;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE Human SNAP-25 peptide #6.
 XX
 KW Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW cosmetic.
 XX
 OS Homo sapiens.
 XX

PN WO2003020948-A2.
XX
PD 13-MAR-2003.
XX
PF 22-AUG-2002; 2002WO-US027145.
XX
PR 28-AUG-2001; 2001US-00942024.
XX
XX (ALLR) ALLERGAN INC.
PA
PI Steward LE, Fernandez-Salas E, Aoki KR;
XX
XX WPI; 2003-290198/28.
XX
XX Botulinum serotype A/E substrate useful for assaying protease activity of
PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
PT toxin recognition sequence that includes a cleavage site.
XX
XX Disclosure; Page 40; 168pp; English.
PS
CC The present invention relates to novel clostridium toxin substrates. The
CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
CC which comprise a donor fluorophore, an acceptor having an absorbance
CC spectrum overlapping the emission spectrum of the donor fluorophore and a
CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
CC the cleavage site intervenes between the donor fluorophore and acceptor
CC and under the appropriate conditions, the resonance energy transfer is
CC exhibited between the donor and acceptor. Natural targets of clostridium
CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
CC of the invention are useful in assaying for the protease activity of any
CC clostridial toxin including botulinum toxins of all serotypes and tetanus
CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
CC samples, water samples, cosmetics, tissue samples and beverage or food
CC samples. They are useful to assay a sample from a human or animal, for
CC e.g., exposed to clostridial toxin or having one or more symptoms of a
CC clostridial toxin, to follow activity during production and purification
CC of clostridial toxin and to assay formulated clostridial toxin products
CC including pharmaceuticals and cosmetics. The present sequence is human
CC SNAP-25 peptide used in the invention
XX
XX Sequence 17 AA;
SQ
Query Match 100.0%; Score 68; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TRIDEANORATKML 15
Db 4 TRIDEANORATKML 17
RESULT 9
ABW01731
ID ABW01731 standard; peptide; 17 AA.
XX
AC ABW01731;
XX
XX 12-FEB-2004 (first entry)
DT
XX Human SNAP-25 BoNT/A recognition peptide #4.
DE
XX Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
XX human.
KW
XX Homo sapiens.
OS
XX US2003143651-A1.
XX
XX 31-JUL-2003.
PD
XX 28-AUG-2001; 2001US-00942098.
PF
XX

PR 28-AUG-2001; 2001US-00942098.
XX
XX (STEW/) STEWARD L E.
PA (FERN/) FERNANDEZ-SALAS E.
PA (AOKI/) AOKI K R.
XX
XX Steward LE, Fernandez-Salas E, Aoki KR;
PI
XX WPI; 2003-829791/77.
XX
XX Determining clostridial toxin protease activity, by treating sample with
PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
PT sequence, under conditions which exhibit resonance energy transfer.
XX
XX Disclosure; Page 10; 0pp; English.
PS
XX The present invention provides clostridial toxin substrates useful in
CC assaying for the protease activity of any clostridial toxin including
CC toxins of all serotypes as well as tetanus toxins. The present sequence
CC is human SNAP-25 BoNT/A (botulinum neurotoxin serotype A) recognition
CC peptide
XX
XX Sequence 17 AA;
SQ
Query Match 100.0%; Score 68; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TRIDEANORATKML 15
Db 4 TRIDEANORATKML 17
RESULT 10
ADM97046
ID ADM97046 standard; peptide; 17 AA.
XX
XX ADM97046;
AC
XX 01-JUL-2004 (first entry)
DT
XX Botulinum toxin substrate recognition sequence #31.
DE
XX Clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.
XX
XX Homo sapiens.
OS
XX WO2004029576-A2.
PN
XX 08-APR-2004.
PD
XX 04-SEP-2003; 2003WO-US028092.
PF
XX 27-SEP-2002; 2002US-00261161.
PR
XX (ALLR) ALLERGAN INC.
PA
XX Fernandez-Salas E, Steward LE, Aoki KR;
PI
XX WPI; 2004-340456/31.
DR
XX Determining clostridial toxin activity, comprises contacting cell with
PT sample comprising substrate with donor fluorophore, acceptor and
PT recognition sequence, exciting fluorophore, and determining resonance
PT energy transfer of contacted cell.
XX
XX Disclosure; SEQ ID NO 52; 188pp; English.
PS
XX The invention relates to a method of determining (M1) clostridial toxin
CC activity, comprising contacting cell with sample comprising clostridial
CC toxin substrate with donor fluorophore (F), acceptor (A) with an
CC absorbance spectrum overlapping emission spectrum of fluorophore
CC clostridial toxin recognition sequence with cleavage site intervening

CC between (F) and (A), where under appropriate conditions resonance
 CC transfer is exhibited between fluorophore and acceptor, exciting the
 CC donor fluorophore, and determining resonance energy transfer of the
 CC contacted cell relative to a control cell, where a difference in
 CC resonance energy transfer of the contacted cell as compared to the
 CC control cell is indicative of clostridial toxin activity. (M1) is useful
 CC for determining clostridial toxin activity, where the sample is a crude
 CC cell lysate, isolated clostridial toxin, formulated clostridial toxin
 CC product, BOTOX or food. (M1) is an automated high-throughput assay. (M1)
 CC reduces the need for animal toxicity studies and serves to analyze
 CC multiple toxin functions such as binding a cellular uptake of the toxin,
 CC translocation into the cell cytosol and protease activity. In the method
 CC M1, the clostridial toxin substrate is a botulinum toxin substrate
 CC selected from a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G
 CC or TeNT substrate comprising a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E,
 CC a recognition sequence for a botulinum toxin used as the clostridial
 CC toxin substrate.
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 68; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
 |||||
 Db 4 TRIDEANQRATKML 17

RESULT 11
 ADM97062
 ID ADM97062 standard; peptide; 17 AA.

XX AC ADM97062;
 XX DT 01-JUL-2004 (first entry)
 XX DE Botulinum toxin substrate recognition sequence #47.
 XX KW clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.
 XX OS Synthetic.
 XX PN W02004029576-A2.
 XX PD 08-APR-2004.
 XX PF 04-SEP-2003; 2003WO-US028092.
 XX PR 27-SEP-2002; 2002US-00261161.
 XX PA (ALLR) ALLERGAN INC.
 XX PI Fernandez-Salas E, Steward LE, Aoki KR;
 XX DR WPI; 2004-340456/31.
 XX PT Determining clostridial toxin activity, comprises contacting cell with
 PT sample comprising substrate with donor fluorophore, acceptor and
 PT recognition sequence, exciting fluorophore, and determining resonance
 PT energy transfer of contacted cell.
 XX PS Disclosure; SEQ ID NO 68; 188pp; English.

XX CC The invention relates to a method of determining (M1) clostridial toxin
 CC activity, comprising contacting cell with sample comprising clostridial
 CC toxin substrate with donor fluorophore (F), acceptor (A) with an
 CC absorbance spectrum overlapping emission spectrum of fluorophore
 CC clostridial toxin recognition sequence with cleavage site intervening
 CC between (F) and (A), where under appropriate conditions resonance
 CC transfer is exhibited between fluorophore and acceptor, exciting the
 CC donor fluorophore, and determining resonance energy transfer of the

CC contacted cell relative to a control cell, where a difference in
 CC resonance energy transfer of the contacted cell as compared to the
 CC control cell is indicative of clostridial toxin activity. (M1) is useful
 CC for determining clostridial toxin activity, where the sample is a crude
 CC cell lysate, isolated clostridial toxin, formulated clostridial toxin
 CC product, BOTOX or food. (M1) is an automated high-throughput assay. (M1)
 CC reduces the need for animal toxicity studies and serves to analyze
 CC multiple toxin functions such as binding a cellular uptake of the toxin,
 CC translocation into the cell cytosol and protease activity. In the method
 CC M1, the clostridial toxin substrate is a botulinum toxin substrate
 CC selected from a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G
 CC or TeNT substrate comprising a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E,
 CC a recognition sequence for a botulinum toxin used as the clostridial
 CC toxin substrate.
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 68; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
 |||||
 Db 4 TRIDEANQRATKML 17

RESULT 12
 AEA14920
 ID AEA14920 standard; peptide; 17 AA.

XX AC AEA14920;
 XX DT 14-JUL-2005 (first entry)
 XX DE Human SNAP-25 substrate BONT/A recognition sequence, SEQ ID NO: 30.
 XX KW Neurotoxin; fluorescence; SNAP-25; botulinum toxin.
 XX OS Homo sapiens.
 XX PN US2005100973-A1.
 XX PD 12-MAY-2005.
 XX PF 13-AUG-2004; 2004US-00917844.
 XX PR 28-AUG-2001; 2001US-00942098.
 XX PA (ALLR) ALLERGAN SALES INC.
 XX PI Steward LE, Gilmore MA, Aoki KR;
 XX DR WPI; 2005-365632/37.
 XX PT Determining clostridial toxin protease activity, by treating sample with
 PT tagged toxin substrate comprising fluorescent protein, first and second
 PT partner of affinity couple and assaying fluorescent cleavage product in
 PT treated sample.
 XX PS Disclosure; SEQ ID NO 30; 97pp; English.

XX CC The present invention relates to a method for determining protease
 CC activity of clostridial neurotoxins such as botulinum neurotoxin (BoNT)
 CC and tetanus neurotoxin (TeNT). The method involves treating with a
 CC sample, in solution phase under conditions suitable for clostridial toxin
 CC protease activity, a tagged toxin substrate (e.g. SNAP-25, VAMP,
 CC syntaxin) comprising fluorescent protein, first partner of affinity
 CC couple and clostridial toxin recognition sequence comprising cleavage
 CC site; contacting treated sample with second partner of affinity couple;
 CC and assaying presence of fluorescent cleavage product in the treated
 CC sample. The present sequence is the human SNAP-25 substrate BONT/A
 CC (botulinum neurotoxin serotype A) recognition sequence.

XX SQ Sequence 17 AA;

Query Match 100.0%; Score 68; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKML 15
 DB 4 TRIDEANORATKML 17

RESULT 13
 AAE36677
 ID AAE36677 standard; peptide; 18 AA.
 XX
 AC AAE36677;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE Human SNAP-25 peptide #8.
 XX
 KW Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW cosmetic.
 XX
 OS Homo sapiens.
 XX
 PN WO2003020948-A2.
 XX
 PD 13-MAR-2003.
 XX
 PF 22-AUG-2002; 2002WO-US027145.
 XX
 PR 28-AUG-2001; 2001US-00942024.
 XX
 PA (ALLR) ALLERGAN INC.
 XX
 PI Steward LE, Fernandez-Salas E, Aoki KR;
 XX
 DR WPI; 2003-290198/28.
 XX
 PT Botulinum serotype A/E substrate useful for assaying protease activity of
 PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 PT toxin recognition sequence that includes a cleavage site.
 XX
 PS Disclosure; Page 40-41; 168pp; English.
 XX
 CC The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance and a
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is human
 CC SNAP-25 peptide used in the invention
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 68; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKML 15
 DB 5 TRIDEANORATKML 18

RESULT 14
 ABW01733
 ID ABW01733 standard; peptide; 18 AA.
 XX
 AC ABW01733;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human SNAP-25 BoNT/A recognition peptide #6.
 XX
 KW Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
 KW human.
 XX
 OS Homo sapiens.
 XX
 PN US2003143651-A1.
 XX
 PD 31-JUL-2003.
 XX
 PF 28-AUG-2001; 2001US-00942098.
 XX
 PR 28-AUG-2001; 2001US-00942098.
 XX
 PA (STEW/) STEWARD L E.
 PA (FERN/) FERNANDEZ-SALAS E.
 PA (AOKI/) AOKI K R.
 XX
 PI Steward LE, Fernandez-Salas E, Aoki KR;
 XX
 DR WPI; 2003-829791/77.
 XX
 PT Determining clostridial toxin protease activity, by treating sample with
 PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
 PT sequence, under conditions which exhibit resonance energy transfer.
 XX
 PS Disclosure; Page 10; Opp; English.
 XX
 CC The present invention provides clostridial toxin substrates useful in
 CC assaying for the protease activity of any clostridial toxin including
 CC toxins of all serotypes as well as tetanus toxins. The present sequence
 CC is human SNAP-25 BoNT/A (botulinum neurotoxin serotype A) recognition
 CC peptide
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 68; DB 7; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKML 15
 DB 5 TRIDEANORATKML 18

RESULT 15
 ADM97048
 ID ADM97048 standard; peptide; 18 AA.
 XX
 AC ADM97048;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Botulinum toxin substrate recognition sequence #33.
 XX
 KW clostridial toxin; fluorophore; clostridial toxin product; BOTOX; food.
 XX

OS Homo sapiens.
 XX
 PN WO2004029576-A2.
 XX
 PD 08-APR-2004.
 XX
 PF 04-SEP-2003; 2003WO-US028092.
 XX
 PR 27-SEP-2002; 2002US-00261161.
 XX
 PA (ALLR) ALLERGAN INC.
 XX
 PI Fernandez-Salas E, Steward LE, Aoki KR;
 XX
 DR WFI; 2004-340456/31.
 XX
 XX Determining clostridial toxin activity, comprises contacting cell with
 PT sample comprising substrate with donor fluorophore, acceptor and
 PT recognition sequence, exciting fluorophore, and determining resonance
 PT energy transfer of contacted cell.
 XX
 XX Disclosure; SEQ ID NO 54; 189pp; English.
 PS
 XX The invention relates to a method of determining (M1) clostridial toxin
 CC activity, comprising contacting cell with sample comprising clostridial
 CC toxin substrate with donor fluorophore (F), acceptor (A) with an
 CC absorbance spectrum overlapping emission spectrum of fluorophore
 CC clostridial toxin recognition sequence with cleavage site intervening
 CC between (F) and (A), where under appropriate conditions resonance
 CC transfer is exhibited between fluorophore and acceptor, exciting the
 CC donor fluorophore, and determining resonance energy transfer of the
 CC contacted cell relative to a control cell, where a difference in
 CC resonance energy transfer of the contacted cell as compared to the
 CC control cell is indicative of clostridial toxin activity. (M1) is useful
 CC for determining clostridial toxin activity, where the sample is a crude
 CC cell lysate, isolated clostridial toxin, formulated clostridial toxin
 CC product, BOTOX or food. (M1) is an automated high-throughput assay. (M1)
 CC reduces the need for animal toxicity studies and serves to analyze
 CC multiple toxin functions such as binding a cellular uptake of the toxin,
 CC translocation into the cell cytosol and protease activity. In the method
 CC M1, the clostridial toxin substrate is a botulinum toxin substrate
 CC selected from a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E, BONT/F, BONT/G
 CC or TEND substrate comprising a BONT/A, BONT/B, BONT/C1, BONT/D, BONT/E,
 CC BONT/F, BONT/G or TEND recognition sequence. This sequence corresponds to
 CC a recognition sequence for a botulinum toxin used as the clostridial
 CC toxin substrate.
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 68; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.6e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKML 15
 |||||
 Db 5 TRIDEANQRATKML 18

Search completed: April 3, 2006, 15:36:57
 Job time : 83.2217 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:49:32 ; Search time 10.1101 Seconds
(without alignments)
57.210 Million cell updates/sec

Title: US-09-942-098-92
Perfect score: 84
Sequence: 1 XTRIDEANQRATKMLGSGX 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDSS5/ptodata/1/pubpaa/US08 NEW_PUB pep.*
2: /SIDSS5/ptodata/1/pubpaa/US06 NEW_PUB pep.*
3: /SIDSS5/ptodata/1/pubpaa/US07 NEW_PUB pep.*
4: /SIDSS5/ptodata/1/pubpaa/US09 NEW_PUB pep.*
5: /SIDSS5/ptodata/1/pubpaa/US05 NEW_PUB pep.*
6: /SIDSS5/ptodata/1/pubpaa/US10 NEW_PUB pep.*
7: /SIDSS5/ptodata/1/pubpaa/US11 NEW_PUB pep.*
8: /SIDSS5/ptodata/1/pubpaa/US60 NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	33	6	US-10-947-071-36
2	84	100.0	33	6	US-10-947-071-40
3	84	100.0	33	6	US-10-947-071-41
4	84	100.0	33	6	US-10-948-097-36
5	84	100.0	33	6	US-10-948-097-40
6	84	100.0	33	6	US-10-948-097-41
7	84	100.0	116	7	US-11-195-098-11
8	84	100.0	203	6	US-10-947-071-4
9	84	100.0	203	6	US-10-948-097-4
10	84	100.0	206	6	US-10-947-071-1
11	84	100.0	206	6	US-10-947-071-2
12	84	100.0	206	6	US-10-948-097-1
13	84	100.0	206	6	US-10-948-097-2
14	84	100.0	206	7	US-11-169-041-225
15	84	100.0	334	6	US-10-947-071-20
16	84	100.0	334	6	US-10-948-097-20
17	78	92.9	116	7	US-11-195-098-12
18	77	91.7	24	7	US-11-195-098-8
19	71	84.5	22	6	US-10-980-346B-1
20	68	81.0	17	6	US-10-980-346B-6
21	68	81.0	17	6	US-10-980-346B-37
22	68	81.0	17	6	US-10-947-071-33
23	68	81.0	17	6	US-10-948-097-33
24	68	81.0	18	6	US-10-947-071-35
25	68	81.0	18	6	US-10-948-097-35

26	65	77.4	17	6	US-10-980-346B-38	Sequence 38, Appl
27	65	77.4	17	6	US-10-947-071-61	Sequence 61, Appl
28	65	77.4	17	6	US-10-948-097-61	Sequence 61, Appl
29	64	76.2	13	6	US-10-947-071-30	Sequence 30, Appl
30	64	76.2	13	6	US-10-948-097-30	Sequence 30, Appl
31	64	76.2	16	6	US-10-947-071-32	Sequence 32, Appl
32	64	76.2	16	6	US-10-948-097-32	Sequence 32, Appl
33	64	76.2	17	6	US-10-947-071-34	Sequence 34, Appl
34	64	76.2	17	6	US-10-947-071-53	Sequence 53, Appl
35	64	76.2	17	6	US-10-947-071-55	Sequence 55, Appl
36	64	76.2	17	6	US-10-947-071-60	Sequence 60, Appl
37	64	76.2	17	6	US-10-948-097-34	Sequence 34, Appl
38	64	76.2	17	6	US-10-948-097-53	Sequence 53, Appl
39	64	76.2	17	6	US-10-948-097-60	Sequence 60, Appl
40	63	75.0	17	6	US-10-947-071-54	Sequence 54, Appl
41	63	75.0	17	6	US-10-947-071-58	Sequence 58, Appl
42	63	75.0	17	6	US-10-947-071-62	Sequence 62, Appl
43	63	75.0	17	6	US-10-948-097-54	Sequence 54, Appl
44	63	75.0	17	6	US-10-948-097-58	Sequence 58, Appl
45	63	75.0	17	6	US-10-948-097-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-10-947-071-36
; Sequence 36, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei
; APPLICANT: Aoki, Kei
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-947-071-36

Query Match	100.0%	Score 84;	DB 6;	Length 33;
Best Local Similarity	100.0%	Pred. No. 7.7e-09;		
Matches	17;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	2	TRIDEANQRATKMLGSG 18		
Db	17	TRIDEANQRATKMLGSG 33		
RESULT 2				
US-10-947-071-40				
; Sequence 40, Application US/10947071				
; Publication No. US20060063221A1				
; GENERAL INFORMATION:				
; APPLICANT: Williams, Dudley J.				
; APPLICANT: Gilmore, Marcella				
; APPLICANT: Steward, Lance				
; APPLICANT: Verhagen, Marc				
; APPLICANT: Aoki, Kei				
; APPLICANT: Aoki, Kei				
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods				
; FILE REFERENCE: 66872-043				
; CURRENT APPLICATION NUMBER: US/10/947,071				
; CURRENT FILING DATE: 2004-09-21				
; NUMBER OF SEQ ID NOS: 101				

```
/ SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-40

Query Match          100.0%; Score 84; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
Db 17 TRIDEANQRATKMLGSG 33

RESULT 3
US-10-947-071-41
; Sequence 41, Application US/10947071
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-41

Query Match          100.0%; Score 84; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
Db 17 TRIDEANQRATKMLGSG 33

RESULT 4
US-10-948-097-36
; Sequence 36, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-948-097-36

Query Match          100.0%; Score 84; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
Db 17 TRIDEANQRATKMLGSG 33

RESULT 5
US-10-948-097-40
; Sequence 40, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-40

Query Match          100.0%; Score 84; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
Db 17 TRIDEANQRATKMLGSG 33

RESULT 6
US-10-948-097-41
; Sequence 41, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-41

Query Match          100.0%; Score 84; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
Db 17 TRIDEANQRATKMLGSG 33

RESULT 7
US-11-195-098-11
```

```
; Sequence 11, Application US/11195098
; Publication No. US20050287622A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/11/195,098
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/802,574
; PRIOR FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 09/962,360
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by Bont E
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-11-195-098-11

Query Match          100.0%; Score 84; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
Db 99 TRIDEANQRATKMLGSG 115

RESULT 8
US-10-947-071-4
; Sequence 4, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-4

Query Match          100.0%; Score 84; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
Db 187 TRIDEANQRATKMLGSG 203

RESULT 9
US-10-948-097-4
```

```
; Sequence 4, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-4

Query Match          100.0%; Score 84; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
Db 187 TRIDEANQRATKMLGSG 203

RESULT 10
US-10-947-071-1
; Sequence 1, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-947-071-1

Query Match          100.0%; Score 84; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
Db 190 TRIDEANQRATKMLGSG 206

RESULT 11
US-10-947-071-2
; Sequence 2, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
```

; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-947-071-2

Query Match 100.0%; Score 84; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKMLGSG 18
|||
DB 190 TRIDEANORATKMLGSG 206

RESULT 12

US-10-948-097-1
; Sequence 1, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:

; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-1

Query Match 100.0%; Score 84; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKMLGSG 18
|||
DB 190 TRIDEANORATKMLGSG 206

RESULT 13

US-10-948-097-2
; Sequence 2, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:

; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT

Query Match 100.0%; Score 84; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; ORGANISM: Mus musculus
US-10-948-097-2

Query Match 100.0%; Score 84; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKMLGSG 18
|||
DB 190 TRIDEANORATKMLGSG 206

RESULT 14

US-11-169-041-225
; Sequence 225, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 225
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-225

Query Match 100.0%; Score 84; DB 7; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKMLGSG 18
|||
DB 190 TRIDEANORATKMLGSG 206

RESULT 15

US-10-947-071-20
; Sequence 20, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:

; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pQBI GFP-SNAP25
US-10-947-071-20

Query Match 100.0%; Score 84; DB 6; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: April 3, 2006, 15:58:09
Job time : 10.1101 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:46:49 ; Search time 81.7523 Seconds
(without alignments)
97.107 Million cell updates/sec

Title: US-09-942-098-92
Perfect score: 84
Sequence: 1 XTRIDEANQRATKMLGSGX 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	19	3	US-09-942-024-92
2	84	100.0	19	3	US-09-942-024-95
3	84	100.0	19	3	US-09-942-098-92
4	84	100.0	19	3	US-09-942-098-95
5	84	100.0	22	3	US-09-942-024-93
6	84	100.0	22	3	US-09-942-098-93
7	84	100.0	23	3	US-09-942-024-88
8	84	100.0	23	3	US-09-942-098-88
9	84	100.0	24	3	US-09-942-024-90
10	84	100.0	24	3	US-09-942-098-90
11	84	100.0	33	3	US-09-942-024-33
12	84	100.0	33	3	US-09-942-024-37
13	84	100.0	33	3	US-09-942-024-38
14	84	100.0	33	3	US-09-942-098-33
15	84	100.0	33	3	US-09-942-098-37
16	84	100.0	33	3	US-09-942-098-38
17	84	100.0	33	4	US-10-261-161-55
18	84	100.0	33	4	US-10-261-161-59
19	84	100.0	33	4	US-10-261-161-60
20	84	100.0	33	5	US-10-917-844-33
21	84	100.0	33	5	US-10-917-844-37
22	84	100.0	33	5	US-10-917-844-38
23	84	100.0	86	4	US-10-705-857-4
24	84	100.0	114	5	US-10-917-844-112
25	84	100.0	116	5	US-09-963-360B-11
26	84	100.0	116	4	US-10-802-574-11
27	84	100.0	203	3	US-09-942-024-14

28	84	100.0	203	3	US-09-942-098-14	Sequence 14, Appli
29	84	100.0	203	4	US-10-261-161-7	Sequence 7, Appli
30	84	100.0	203	5	US-10-917-844-14	Sequence 14, Appli
31	84	100.0	206	3	US-09-942-024-2	Sequence 2, Appli
32	84	100.0	206	3	US-09-942-024-7	Sequence 7, Appli
33	84	100.0	206	3	US-09-942-024-12	Sequence 12, Appli
34	84	100.0	206	3	US-09-942-098-2	Sequence 2, Appli
35	84	100.0	206	3	US-09-942-098-7	Sequence 7, Appli
36	84	100.0	206	3	US-09-942-098-12	Sequence 12, Appli
37	84	100.0	206	4	US-10-261-161-4	Sequence 4, Appli
38	84	100.0	206	4	US-10-261-161-5	Sequence 5, Appli
39	84	100.0	206	4	US-10-261-161-109	Sequence 109, App
40	84	100.0	206	4	US-10-318-417-3	Sequence 3, Appli
41	84	100.0	206	5	US-10-723-860-1223	Sequence 1223, Ap
42	84	100.0	206	5	US-10-917-844-2	Sequence 2, Appli
43	84	100.0	206	5	US-10-917-844-12	Sequence 12, Appli
44	84	100.0	206	5	US-10-917-844-90	Sequence 90, Appli
45	84	100.0	206	5	US-10-756-149-5012	Sequence 5012, Ap

ALIGNMENTS

RESULT 1
US-09-942-024-92
; Sequence 92, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28.
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 19
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-92

Query Match 100.0%; Score 84; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
|
Db 2 TRIDEANQRATKMLGSG 18

RESULT 2
US-09-942-024-95
; Sequence 95, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum

```
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=DABCYL modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 19
; OTHER INFORMATION: Xaa=EDANS modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-95
```

```
Query Match 100.0%; Score 84; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
||| ||||| ||||| |||
Db 2 TRIDEANQRATKMLGSG 18
```

```
RESULT 3
US-09-942-098-92
; Sequence 92, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa-fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 19
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-92

Query Match 100.0%; Score 84; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
||| ||||| ||||| |||
Db 2 TRIDEANQRATKMLGSG 18
```

```
RESULT 4
US-09-942-098-95
; Sequence 95, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=DABCYL modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 19
; OTHER INFORMATION: Xaa=EDANS modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-95
```

```
Query Match 100.0%; Score 84; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
||| ||||| ||||| |||
Db 2 TRIDEANQRATKMLGSG 18
```

```
RESULT 5
US-09-942-024-93
; Sequence 93, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa-fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 22
; OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-93
```

Query Match 100.0%; Score 84; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
|||||
Db 5 TRIDEANQRATKMLGSG 21

RESULT 6
US-09-942-098-93
; Sequence 93, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 22
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-93

Query Match 100.0%; Score 84; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
|||||
Db 5 TRIDEANQRATKMLGSG 21

RESULT 7
US-09-942-024-88
; Sequence 88, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1

; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 23
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-88

Query Match 100.0%; Score 84; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
|||||
Db 6 TRIDEANQRATKMLGSG 22

RESULT 8
US-09-942-098-88
; Sequence 88, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 23
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-88

Query Match 100.0%; Score 84; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
|||||
Db 6 TRIDEANQRATKMLGSG 22

RESULT 9
US-09-942-024-90
; Sequence 90, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa-fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 24
; OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
; US-09-942-024-90
```

```
Query Match 100.0%; Score 84; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 TRIDEANQRATKMLGSG 18
| | | | | | | | | | | | | | | | | |
Db 7 TRIDEANQRATKMLGSG 23
```

```
RESULT 10
US-09-942-098-90
; Sequence 90, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa-fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 24
; OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
; US-09-942-098-90
```

```
Query Match 100.0%; Score 84; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 TRIDEANQRATKMLGSG 18
| | | | | | | | | | | | | | | | | |
Db 7 TRIDEANQRATKMLGSG 23
```

```
RESULT 11
US-09-942-024-33
; Sequence 33, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: Serotype A/E Toxins
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-942-024-33
```

```
Query Match 100.0%; Score 84; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 TRIDEANQRATKMLGSG 18
| | | | | | | | | | | | | | | | | |
Db 17 TRIDEANQRATKMLGSG 33
```

```
RESULT 12
US-09-942-024-37
; Sequence 37, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: Serotype A/E Toxins
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
; US-09-942-024-37
```

```
Query Match 100.0%; Score 84; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 TRIDEANQRATKMLGSG 18
| | | | | | | | | | | | | | | | | |
Db 17 TRIDEANQRATKMLGSG 33
```

```
RESULT 13
US-09-942-024-38
; Sequence 38, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: Serotype A/E Toxins
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 33
; TYPE: PRT
```

Job time : 82.7523 secs

```
; ORGANISM: Carassius auratus
US-09-942-024-38

Query Match      100.0%; Score 84; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TRIDEANQRATKMLGSG 18
Db      17 TRIDEANQRATKMLGSG 33

RESULT 14
US-09-942-098-33
; Sequence 33, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Pret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-33

Query Match      100.0%; Score 84; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TRIDEANQRATKMLGSG 18
Db      17 TRIDEANQRATKMLGSG 33

RESULT 15
US-09-942-098-37
; Sequence 37, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Pret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-098-37

Query Match      100.0%; Score 84; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TRIDEANQRATKMLGSG 18
Db      17 TRIDEANQRATKMLGSG 33

Search completed: April 3, 2006, 15:57:06
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:31:39 ; Search time 15.1651 Seconds
(without alignments)
103.582 Million cell updates/sec

Title: US-09-942-098-92
Perfect score: 84
Sequence: 1 XTRIDEANQRATKMLGSGX 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCRUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	20	2	US-08-819-286-9
2	84	100.0	26	2	US-08-819-286-8
3	84	100.0	37	2	US-08-819-286-4
4	84	100.0	70	1	US-08-760-001-10
5	84	100.0	70	2	US-08-015-960-10
6	84	100.0	70	2	US-09-534-572-10
7	84	100.0	116	2	US-08-962-360B-11
8	84	100.0	206	1	US-08-393-985-18
9	84	100.0	206	2	US-08-819-286-1
10	84	100.0	206	2	US-09-943-016-6311
11	84	100.0	219	2	US-09-943-016-10671
12	78	92.9	116	2	US-09-962-360B-12
13	77	91.7	24	2	US-09-962-360B-8
14	68	81.0	17	1	US-08-743-894B-1
15	68	81.0	17	1	US-08-743-894B-37
16	65	77.4	17	1	US-08-743-894B-2
17	65	77.4	17	1	US-08-743-894B-18
18	65	77.4	17	1	US-08-743-894B-43
19	64	76.2	13	2	US-09-976-535A-1
20	64	76.2	16	1	US-08-743-894B-49
21	64	76.2	17	1	US-08-743-894B-27
22	64	76.2	17	1	US-08-743-894B-30
23	64	76.2	17	1	US-08-743-894B-32
24	64	76.2	17	1	US-08-743-894B-39
25	63	75.0	17	1	US-08-743-894B-19
26	63	75.0	17	1	US-08-743-894B-25
27	63	75.0	17	1	US-08-743-894B-29

28	63	75.0	17	1	US-08-743-894B-42	Sequence 42, Appl
29	63	75.0	17	1	US-08-743-894B-50	Sequence 50, Appl
30	62	73.8	17	1	US-08-743-894B-3	Sequence 3, Appl
31	62	73.8	17	1	US-08-743-894B-20	Sequence 20, Appl
32	62	73.8	17	1	US-08-743-894B-24	Sequence 24, Appl
33	62	73.8	17	1	US-08-743-894B-26	Sequence 26, Appl
34	62	73.8	17	1	US-08-743-894B-28	Sequence 28, Appl
35	62	73.8	17	1	US-08-743-894B-31	Sequence 31, Appl
36	62	73.8	17	1	US-08-743-894B-33	Sequence 33, Appl
37	62	73.8	17	1	US-08-743-894B-34	Sequence 34, Appl
38	62	73.8	17	1	US-08-743-894B-36	Sequence 36, Appl
39	62	73.8	17	1	US-08-743-894B-44	Sequence 44, Appl
40	62	73.8	17	1	US-08-743-894B-45	Sequence 45, Appl
41	62	73.8	17	1	US-08-743-894B-46	Sequence 46, Appl
42	61	72.6	13	1	US-08-743-894B-16	Sequence 16, Appl
43	61	72.6	14	2	US-09-976-535A-2	Sequence 2, Appl
44	61	72.6	16	1	US-08-743-894B-51	Sequence 51, Appl
45	61	72.6	17	1	US-08-743-894B-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-819-286-9
; Sequence 9, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-9

Query Match 100.0%; Score 84; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
|||||

```
Db          4  TRIDEANQRATKMLGSG 20

RESULT 2
US-08-819-286-8
; Sequence 8, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montcal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; APPLICATION NUMBER: US/08/819,286-4
; US-08-819-286-4

Query Match 100.0%; Score 84; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2  TRIDEANQRATKMLGSG 18
Db          21  TRIDEANQRATKMLGSG 37

RESULT 4
US-08-760-001-10
; Sequence 10, Application US/08760001
; Patent No. 5962637
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,001
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543

Qy          2  TRIDEANQRATKMLGSG 18
Db          10  TRIDEANQRATKMLGSG 26

RESULT 3
US-08-819-286-4
; Sequence 4, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montcal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
```

INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 70 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-760-001-10

Query Match 100.0%; Score 84; DB 1; Length 70;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
 Db 54 TRIDEANQRATKMLGSG 70

RESULT 5
 US-09-015-960-10
 ; Sequence 10, Application US/09015960
 ; Patent No. 6043042
 ; GENERAL INFORMATION:
 ; APPLICANT: Shone, Clifford C.
 ; APPLICANT: Hallis, Bassam
 ; APPLICANT: James, Benjamin A. F.
 ; APPLICANT: Quinn, Conrad P.
 ; TITLE OF INVENTION: TOXIN ASSAY
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 ; STREET: 1100 New York Ave., N.W., Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/015,960
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/760,001
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Esmond, Robert W.
 ; REGISTRATION NUMBER: 32,893
 ; REFERENCE/DOCKET NUMBER: 1581.0120001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2543
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 70 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-015-960-10

Query Match 100.0%; Score 84; DB 2; Length 70;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
 Db 54 TRIDEANQRATKMLGSG 70

RESULT 6
 US-09-534-572-10
 ; Sequence 10, Application US/09534572
 ; Patent No. 6337386
 ; GENERAL INFORMATION:
 ; APPLICANT: Shone, Clifford C.
 ; APPLICANT: Hallis, Bassam
 ; APPLICANT: James, Benjamin A. F.
 ; APPLICANT: Quinn, Conrad P.
 ; TITLE OF INVENTION: TOXIN ASSAY
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 ; STREET: 1100 New York Ave., N.W., Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/534,572
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/015,960
 ; FILING DATE: 30-JAN-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/760,001
 ; FILING DATE: 30-DEC-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB95/01279
 ; FILING DATE: 02-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Esmond, Robert W.
 ; REGISTRATION NUMBER: 32,893
 ; REFERENCE/DOCKET NUMBER: 1581.0120003
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2543
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 70 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-534-572-10

Query Match 100.0%; Score 84; DB 2; Length 70;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
 Db 54 TRIDEANQRATKMLGSG 70

RESULT 7
 US-09-962-360B-11
 ; Sequence 11, Application US/09962360B
 ; Patent No. 6762280
 ; GENERAL INFORMATION:
 ; APPLICANT: Schmidt, James J.
 ; APPLICANT: Stafford, Robert G.
 ; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
 ; TITLE OF INVENTION: Neurotoxins
 ; FILE REFERENCE: 003/224/SAP
 ; CURRENT APPLICATION NUMBER: US/09/962,360B

```
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
; US-09-962-360B-11

Query Match 100.0%; Score 84; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
||| ||||| ||||| |||||
Db 99 TRIDEANQRATKMLGSG 115

RESULT 8
US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Scheller, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-393-985-18

Query Match 100.0%; Score 84; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
||| ||||| ||||| |||||
Db 190 TRIDEANQRATKMLGSG 206
```

```
RESULT 9
US-08-819-286-1
; Sequence 1, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-1

Query Match 100.0%; Score 84; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
||| ||||| ||||| |||||
Db 190 TRIDEANQRATKMLGSG 206

RESULT 10
US-09-949-016-6311
; Sequence 6311, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6311
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6311

Query Match 100.0%; Score 84; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 190 TRIDEANQRATKMLGSG 206

RESULT 11
US-09-949-016-10671
; Sequence 10671, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10671
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10671

Query Match 100.0%; Score 84; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 9.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 203 TRIDEANQRATKMLGSG 219

RESULT 12
US-09-962-360B-12
; Sequence 12, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 12
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E.

Query Match 91.7%; Score 77; DB 2; Length 24;
Best Local Similarity 88.2%; Pred. No. 1.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 7 TRIDEANQRATKMLGSG 23

RESULT 14
US-08-743-894B-1
; Sequence 1, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn: John Moran-Patent Atty
; STREET: USA WPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0

Query Match 92.9%; Score 78; DB 2; Length 116;
Best Local Similarity 94.1%; Pred. No. 5.2e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 99 TRIDEANQRATKMLGSG 115

RESULT 13
US-09-962-360B-8
; Sequence 8, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 8
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT A

Query Match 91.7%; Score 77; DB 2; Length 24;
Best Local Similarity 88.2%; Pred. No. 1.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 7 TRIDEANQRATKMLGSG 23

RESULT 14
US-08-743-894B-1
; Sequence 1, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn: John Moran-Patent Atty
; STREET: USA WPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0

```

; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
US-08-743-894B-1

Query Match 81.0%; Score 68; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15
Db 4 TRIDEANQRATKML 17

RESULT 15
US-08-743-894B-37
; Sequence 37, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MEMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;

```

```

; FEATURE:
; US-08-743-894B-37

Query Match 81.0%; Score 68; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKML 15
Db 4 TRIDEANQRATKML 17

Search completed: April 3, 2006, 15:33:15
Job time : 15.1651 secs

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:27:42 ; Search time 97.9633 Seconds
(without alignments)
136.837 Million cell updates/sec

Title: US-09-942-098-92
Perfect score: 84
Sequence: 1 XTRIDEANQRATKMLGSGX 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	124	2	Q93578 BRARE
2	84	100.0	134	2	Q48855 TETNG
3	84	100.0	143	2	Q9GM34 MACFA
4	84	100.0	198	2	Q6PC84 BRARE
5	84	100.0	203	1	SN25B CARAU
6	84	100.0	203	2	Q93579 BRARE
7	84	100.0	203	2	Q93579 BRARE
8	84	100.0	204	1	SN25A CARAU
9	84	100.0	204	2	Q705J6 LATJA
10	84	100.0	204	2	Q5TZ66 BRARE
11	84	100.0	204	2	Q5TZ65 BRARE
12	84	100.0	206	1	SN25 CHICK
13	84	100.0	206	1	SNP25 HUMAN
14	84	100.0	206	1	SNP25 MACMU
15	84	100.0	206	1	SNP25 PANTR
16	84	100.0	206	1	SNP25 RAT
17	84	100.0	206	2	Q5JEM2 HUMAN
18	84	100.0	206	2	Q5U0B5 HUMAN
19	84	100.0	206	2	Q5NVG5 PONPY
20	84	100.0	206	2	Q5NVK3 PONPY
21	84	100.0	206	2	Q5R690 PONPY
22	84	100.0	206	2	Q5R6U7 PONPY
23	84	100.0	206	2	Q4R4U6 MACFA
24	84	100.0	206	2	Q4VS09 CARAU
25	84	100.0	236	2	Q6P3L7 BRARE
26	80	95.2	204	2	Q6P3L7 BRARE
27	77	91.7	206	2	Q5R505 PONPY
28	70	83.3	206	2	Q640W4 XENLA
29	70	83.3	206	2	Q8AXM1 XENLA
30	70	83.3	206	2	Q8AXM2 XENLA
31	55	65.5	214	2	Q7ZVE4 BRARE

32	54	64.3	137	2	Q66ID7 BRARE	Q66id7 brachydanio
33	54	64.3	186	2	Q4V9B7 BRARE	Q4v9b7 brachydanio
34	54	64.3	209	2	Q4V9B6 BRARE	Q4v9b6 brachydanio
35	54	64.3	210	1	SNP25 TORMA	P36976 torpedo peal
36	54	64.3	212	2	Q8T3S4 LOLPE	Q8t3s4 loligo peal
37	53	63.1	230	2	Q4REP6 TETNG	Q4rep6 tetraodon n
38	48	57.1	204	2	Q8JIS7 XENLA	Q8jis7 xenopus lae
39	47	56.0	114	2	Q8CAK0 MOUSE	Q8cak0 mus musculus
40	46	54.8	220	2	Q869G6 LYMTS	Q869g6 lymnaea sta
41	46	54.8	771	2	Q9XZJ3 DICDI	Q9xzj3 dictyostell
42	46	54.8	907	2	Q9FJE6 ARATH	Q9fje6 arabidopsis
43	46	54.8	1361	1	RPOC2 SPIOL	P11704 spinacia ol
44	45	53.6	83	2	O85431 PSESD	O85431 pseudomonas
45	45	53.6	83	2	O85439 PSEFL	O85439 pseudomonas

ALIGNMENTS

RESULT 1
O93578 BRARE
ID O93578 BRARE PRELIMINARY; PRT; 124 AA.
AC O93578; 01-NOV-1998 (TREMREL. 08, Created)
DT 01-NOV-1998 (TREMREL. 08, Last sequence update)
DE Synaptochrome-associated protein 25.1 (Fragment).
GN Names-snap25a; Synonyms-Snap;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99057281; PubMed=98431147;
RY DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNR1>3.3.CO;2-Z;
RL EMBL; AF091593; AAC64289.1; -; mRNA.
DR HSP; Q8T3S4; 1L4A.
DR SMR; Q93578; 49-122.
DR Ensembl; ENSDARG0000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR GO; GO:0019717; C:synaptochrome; IEA.
DR GO; GO:0003700; P:regulation of transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002197; WH Fis.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR PRINTS; PR01590; HTHFIS.
DR SMART; SM00397; t-SNARE; 1.
DR PROSITE; PS50192; t-SNARE; 1.
DR Synaptochrome.
FT NON TER
SQ SEQUENCE 124 AA; 13616 MW; 50E27DBDB33D958C CRC64;

Query Match 100.0%; Score 84; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TRIDEANQRATKMLGSG 18
Db 108 TRIDEANQRATKMLGSG 124
RESULT 2

1

KW Synaptosome.
SQ SEQUENCE 198 AA; 22209 MW; 8FED5099A00E1EC0 CRC64;

Query Match 100.0%; Score 84; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKMLGSG 18
DB 182 TRIDEANORATKMLGSG 198

RESULT 5
SN25B_CARAU STANDARD; PRT; 203 AA.
AC P36978;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptosome-associated protein 25B (SNAP-25B).
GN Name=SNAP-B;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RX MEDLINE=94068448; PubMed=8248151;
RA Risinger C., Lahammar D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish."
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC -1- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
CC -1- SUBCELLULAR LOCATION: Complexed with macromolecular elements of the nerve terminal.
CC -1- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, piriform cortex, anterior thalamic nuclei, pontine nuclei, and granule cells of the cerebellum.
CC -1- SIMILARITY: Belongs to the SNAP-25 family.
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

EMBL; L22976; AAA16538.1; -; mRNA.
PIR; I50481; I50481.
HSP; P13795; 18FC.
SMR; P36978; 7-82, 128-201.
InterPro; IPR000928; SNAP-25.
InterPro; IPR000727; T-SNARE.
Pfam; PF00835; SNAP-25; 1.
Pfam; PF05739; SNAP-25; 1.
SMART; SM00397; t-SNARE; 2.
PROSITE; PS50192; t-SNARE; 2.
Coiled coil; Glycoprotein; Multigene family; Repeat; Synaptosome.
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 137 199 t-SNARE coiled-coil homology 2.
FT COMPBIAS 85 92 Cys-rich.
FT CARBOHYD 77 77 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 185 185 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 203 AA; 22664 MW; 8DFBDBED37D6D7 CRC64;

Query Match 100.0%; Score 84; DB 1; Length 203;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKMLGSG 18
DB 187 TRIDEANORATKMLGSG 203

RESULT 6
O93579 BRARE PRELIMINARY; PRT; 203 AA.
AC O93579;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein 25.2.
GN Name=snap25b; Synonyms=Snap;
OS Brachydanio rerio (Zebrafish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99057281; PubMed=9843147;
RX DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNRI>3.3.CO;2-Z;
RA Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H., Larhammar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish: comparison of paralogous linkage groups suggests loss of one locus in the mammalian lineage";
RL J. Neurosci. Res. 54:563-573(1998).
DR HSP; P60881; 1JTH.
DR SMR; O93579; 7-82, 128-201.
DR ZFIN; ZDB-GENE-980526-392; snap25b.
GO; GO:0019171; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; T-SNARE; 2.
KW Synaptosome.
SQ SEQUENCE 203 AA; 22647 MW; 93B7590DD0C93F38 CRC64;

Query Match 100.0%; Score 84; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKMLGSG 18
DB 187 TRIDEANORATKMLGSG 203

RESULT 7
O6PC54 BRARE PRELIMINARY; PRT; 203 AA.
AC O6PC54;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Synaptosome-associated protein 25 b.
GN Name=snap25b;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wild-type; TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Wild-type; TISSUE=Eye;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059469; AAHS9469.1; -; mRNA.
DR SNR; Q6PC54; 7-82, 128-201.
DR ZFIN; ZDB-GENE-980526-392; snap25b.
DR GO; GO:0019717; C:synaptoosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
KW Synaptoosome.
SQ SEQUENCE 203 AA; 22693 MW; 48D7590DD0C1179A CRC64;
Query Match 100.0%; Score 84; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TRIDEANORATKMLGSG 18
DB 187 TRIDEANORATKMLGSG 203
|||||
RESULT 8
ID SN25A_CARAU STANDARD; PRT; 204 AA.
AC P36977;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptoosomal-associated protein 25A (SNAP-25A).
GN Name=SNAP-A;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Retina;
RX MEDLINE=94068448; PubMed=8248151;
RA Risinger C., Larnham D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid
RT goldfish.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC -I- FUNCTION: May play an important role in the synaptic function of
CC specific neuronal systems. Associates with proteins involved in
CC vesicle docking and membrane fusion.
CC -I- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
CC the nerve terminal.
CC -I- SIMILARITY: Belongs to the SNAP-25 family.
CC -I- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; L22973; AAA16537.1; -; mRNA.
DR PIR; I50480; I50480.
DR HSSP; P13795; 1N7S.
DR SNR; P36977; 7-83, 129-202.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
KW Coiled coil; Multigene family; Repeat; Synaptoosome.
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 138 200 t-SNARE coiled-coil homology 2.
FT COMPBIAS 85 92 Cys-rich.
SQ SEQUENCE 204 AA; 22843 MW; 458BBECFCFC09189 CRC64;
Query Match 100.0%; Score 84; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TRIDEANORATKMLGSG 18
DB 188 TRIDEANORATKMLGSG 204
|||||
RESULT 9
ID Q705J6_LATJA PRELIMINARY; PRT; 204 AA.
AC Q705J6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Synaptoosomal-associated protein 25.
GN Name=snap-25;
OS Lateolabrax japonicus (Japanese sea perch) (Japanese sea bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Lateolabrax.
OX NCBI_TaxID=8164;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RA Chen K., Huang X.H.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ619993; CAP04071.1; -; mRNA.
DR SNR; Q705J6; 7-83, 129-202.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 204 AA; 22842 MW; 8F77B18D591509B2 CRC64;
Query Match 100.0%; Score 84; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TRIDEANORATKMLGSG 18
DB 188 TRIDEANORATKMLGSG 204
|||||

```
RESULT 10
Q5TZ66 BRARE
ID Q5TZ66 BRARE PRELIMINARY; PRT; 204 AA.
AC Q5TZ66;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Synaptoosomal-associated protein (SNAP).
GN Name=snap25a; Synonyms=OTTDARPO000005563; ORFNames=DKEVP-8F4.6-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lovell J.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Donaldson S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX465184; CAI21360.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69031.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69031.1; -; Genomic DNA.
DR EMBL; BX465184; CAI21359.1; JOINED; Genomic DNA.
DR SMR; Q5TZ66; 7-83, 129-202.
DR Ensembl; ENSDARG0000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR GO; GO:0019717; C:synaptoosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS0192; T_SNARE; 2.
KW Synaptoosome.
SQ SEQUENCE 204 AA; 22878 MW; B53CF5F3D1C69EA5 CRC64;

Query Match 100.0%; Score 84; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
DB 188 TRIDEANQRATKMLGSG 204

RESULT 12
SNP25_CHICK
ID SNP25_CHICK STANDARD; PRT; 206 AA.
AC P60878; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptoosomal-associated protein 25 (SNAP-25) (Synaptoosomal-associated
DE 25 kDa protein) (Super protein) (SUP).
GN Name=SNAP25; Synonyms=SNAP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM SNAP25B).
RC STRAIN=White leghorn; TISSUE=Retina;
RX MEDLINE=91126080; PubMed=1992470;
RA Catsicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,
RA Wilson M.C.;
RA "Expression of a conserved cell-type-specific protein in nerve
RT terminals coincides with synaptogenesis."
RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS SNAP25A AND SNAP25B).
RX MEDLINE=93389738; PubMed=8377193;
RA Bark I.C.;
RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon
RT encoding distinct isoforms of the protein."
RL J. Mol. Biol. 233:67-76(1993).
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion (By
CC similarity).
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1
CC and SNAP25BP. Binds STXBPE. Found in a ternary complex with STX1A
CC and VAMP8 (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60878-1, P13795-1;
CC Sequence=Displayed;
CC Name=SNAP-25a;
CC IsoId=P60878-2, P13795-2;
```

```
CC      Sequence=VSP_010018;
CC      -|- PTM: Palmitoylated (By similarity).
CC      -|- SIMILARITY: Belongs to the SNAP-25 family.
CC      -|- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; M57957; AAA49070.1; -; mRNA.
DR      EMBL; L09253; AAA49070.1; -; Genomic DNA.
DR      EMBL; L09254; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09257; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09259; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09251; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09258; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09250; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09253; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09254; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09257; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09259; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09252; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09258; AAA49070.1; JOINED; Genomic DNA.
DR      EMBL; L09250; AAA49070.1; JOINED; Genomic DNA.
DR      PIR; A37861; A37861.
DR      DNR; P60878; 7-83, 131-204.
DR      InterPro; IPR000928; SNAP-25.
DR      InterPro; IPR000727; T SNARE.
DR      Pfam; PF00835; SNAP-25_1.
DR      Pfam; PF05739; SNARE; 1.
DR      SMART; SM00397; t SNARE; 2.
DR      PROSITE; PS50192; T SNARE; 2.
KW      Alternative splicing; Coiled coil; Lipoprotein; Palmitate;
KW      Phosphorylation; Repeat; Synaptosome.
FT      DOMAIN 19 81
FT      t-SNARE coiled-coil homology 1.
FT      DOMAIN 140 202
FT      t-SNARE coiled-coil homology 2.
FT      COMPBIAS 85 92
FT      Cys-rich.
FT      SITE 180 181
FT      Cleavage (by BONT/E) (By similarity).
FT      MOD_RES 138 138
FT      Phosphoserine (By similarity).
FT      MOD_RES 187 187
FT      ERIEENGNDQINKMKAEKNLTDLGKFCGLCV -> DRVVEE
FT      VARSPPLIC 58 89
FT      GMHINQDMKEAKENLKLGLKCCGLFI (in isoform
FT      SNAP-25a).
FT      /FTID=VSP_010018.
FT      SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
Query Match 100.0%; Score 84; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2 TRIDEANQRATKMLGSG 18
Db      |||||
Db      190 TRIDEANQRATKMLGSG 206
RESULT 13
SNP25_HUMAN STANDARD; PRT; 206 AA.
AC P60880; F13795; P36974; P70558; Q8IXK3; Q96FW2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (synaptosomal-associated
DE 25 kDa protein) (Super protein) (SUP).
GN Name=SNAP25; Synonyms=SNAP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
```

```
RP      NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A AND SNAP-25B).
RC      TISSUE=Brain;
RX      MEDLINE=94156217; PubMed=8112622; DOI=10.1016/0378-1119(94)90773-0;
RA      Bark I.C., Wilson M.C.;
RT      "Human cDNA clones encoding two different isoforms of the nerve
RT      terminal protein SNAP-25."
RL      Gene 139:291-292(1994).
RN      [2]
RP      NUCLEOTIDE SEQUENCE (ISOFORMS SNAP-25A).
RC      TISSUE=Brain;
RX      MEDLINE=94333829; PubMed=8056350; DOI=10.1016/0378-1119(94)90027-2;
RA      Zhao N., Hashida H., Takahashi N., Sakaki Y.;
RT      "Cloning and sequence analysis of the human SNAP25 cDNA."
RL      Gene 145:313-314(1994).
RN      [3]
RP      NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.
RC      TISSUE=Skeletal muscle;
RX      MEDLINE=96332494; PubMed=8760387;
RA      Jagadeish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H.,
RA      Grigovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J.,
RA      Ward C.W.;
RT      "Insulin-responsive tissues contain the core complex protein SNAP-25
RT      (synaptosomal-associated protein 25) A and B isoforms in addition to
RT      syntaxin 4 and synaptobrevins 1 and 2."
RL      Biochem. J. 317:945-954(1996).
RN      [4]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX      MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA      Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA      Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA      Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA      Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA      Buck D., Burrill W.D., Bucler A.P., Carder C., Carter N.P.,
RA      Clegg S., Cobley V.E., Collier R.E., Connor R.E., Clark S.Y., Clee C.M.,
RA      Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA      Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA      Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA      Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA      Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA      Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA      Lechvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA      Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
RA      Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA      Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA      Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA      Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
RA      Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA      Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA      Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA      Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA      Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA      Rogers J.;
RT      "The DNA sequence and comparative analysis of human chromosome 20."
RL      Nature 414:865-871(2001).
RN      [5]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25A).
RC      TISSUE=Eye;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Sapleton M., Soares M.B., Bonaldo M.F., Casavani T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA      Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
```

Ra Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Ra Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Ra Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 11-81 AND 141-202 IN COMPLEX
RP WITH STX1A; CPLX1 AND VAMP2, AND NMR ANALYSIS
RP MEDLINE=21822661; PubMed=11832227; DOI=10.1016/S0896-6273(02)00583-4;
RX Chen X., Tomchick D.R., Kovrig E., Arac D., Machius M.,
RT Suedhof T.C., Rizo J.;
RA "Three-dimensional structure of the complexin/SNARE complex.";
RL Neuron 33:397-409(2002).
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion.
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
CC SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with
CC STX1A and VAMP8 (By similarity).
CC -1- INTERACTION:
CC Q8IUH5:HIP14; NbExp=1; IntAct=EBI-524785, EBI-524753;
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=isoforms differ by the usage of two alternative
CC homologous exons (5a and 5b) which encode for positions 56 to 94
CC and differ only in 9 positions out of 39;
CC Name=SNAP-25b;
CC IsoId=P60880-1, P13795-1;
CC Sequence=displayed;
CC Name=SNAP-25a;
CC IsoId=P60880-2, P13795-2;
CC Sequence=VSP_006186;
CC -1- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, and
CC piriform cortex, anterior thalamic nuclei, pontine nuclei, and
CC granule cells of the cerebellum.
CC -1- PTM: Palmitoylated (By similarity).
CC -1- SIMILARITY: Belongs to the SNAP-25 family.
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; L19760; AAC37545.1; -; mRNA.
CC EMBL; L19761; AAC37546.1; -; mRNA.
CC EMBL; D21267; BAA22370.1; -; mRNA.
CC EMBL; AL023913; CAC34534.1; -; Genomic DNA.
CC EMBL; AL023913; CAC34535.1; -; Genomic DNA.
CC EMBL; AL023913; CAD56158.1; -; Genomic DNA.
CC EMBL; AL023913; CAB42860.1; -; Genomic DNA.
CC EMBL; BC010647; AAH10647.1; -; mRNA.
CC PIR; I53735; I53735.
CC PIR; I67823; I67823.
CC PDB; 1KIL; X-ray; C=11-80, D=141-203.
CC PDB; 1XTG; X-ray; B=146-204.
CC SMR; P60880; 7-83, 131-204.
CC IntAct; P60880; -;
CC Ensemble; ENSG00000132639; Homo sapiens.
CC HGNC; HGNC:11132; SNAP25.
CC H-InvDB; HIX0015639; -;
CC MIM; 600322; -;
CC GO; GO:0007269; P:neurotransmitter secretion; NAS.
CC GO; GO:0001504; P:neurotransmitter uptake; NAS.
CC GO; GO:0050796; P:regulation of insulin secretion; TAS.
CC GO; GO:0007268; P:synaptic transmission; NAS.
CC GO; GO:0016081; P:synaptic vesicle docking during exocytosis; NAS.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T_SNARE.

DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS0192; t-SNARE; 2.
KW 3D-structure; Alternative splicing; Coiled coil; Lipoprotein;
KW Palmitate; Phosphorylation; Repeat; Synaptosome.
FT DOMAIN 19 81
FT t-SNARE coiled-coil homology 1.
FT t-SNARE coiled-coil homology 2.
FT Cys-rich.
FT SITE 85 92
FT Cleavage (by BONT/E).
FT SITE 180 181
FT Phosphothreonine (By similarity).
FT MOD_RES 138 138
FT Phosphoserine (By similarity).
FT MOD_RES 187 187
FT ERIEGMDQINKDKAEKNLDTLGEKGLCV -> DRVVEE
FT VARSPPLIC 58 89
FT GMNHINQDMKEAKNLDLKKCCGLFI (in isoform
FT SNAP-25a).
FT /FTId=VSP_006186.
FT
FT HELIX 7 82
FT HELIX 142 201
FT TURN 202 202
SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
Query Match 100.0%; Score 84; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TRIDEANQRATKMLGSG 18
DB 190 TRIDEANQRATKMLGSG 206
|||||
RESULT 14
SNP25 MACMU STANDARD; PRT; 206 AA.
ID AC P6087; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
DE 25 kDa protein).
GN Name=SNAP25;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Hippocampus;
RA Jensen M.J., Smith L.A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
CC neurotransmitter release. May play an important role in the
CC synaptic function of specific neuronal systems. Associates with
CC proteins involved in vesicle docking and membrane fusion (By
CC similarity).
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
CC SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with
CC STX1A and VAMP8 (By similarity).
CC -1- PTM: Palmitoylated (By similarity).
CC -1- SIMILARITY: Belongs to the SNAP-25 family.
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AF240770; AAF64477.1; -; mRNA.
CC SMR; P60877; 7-83, 131-204.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T_SNARE.

DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t_SNARE; 2.
 DR PROSITE; PS0192; t_SNARE; 2.
 KW Coiled coil; Lipoprotein; Palmitate; Phosphorylation; Repeat;
 KW Synaptosome.
 FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
 FT DOMAIN 140 202 t-SNARE coiled-coil homology 2.
 FT COMPIAS 85 92 Cys-rich.
 FT SITE 180 181 Cleavage (by BONT/E) (By similarity).
 FT MOD_RES 138 138 Phosphothreonine (By similarity).
 FT MOD_RES 187 187 Phosphoserine (By similarity).
 SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;
 Query Match 100.0%; Score 84; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. NO. 7.4e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TRIDEANQRATKMLGSG 18
 DB 190 TRIDEANQRATKMLGSG 206
 RESULT 15
 SNP25 MOUSE STANDARD; PRT; 206 AA.
 ID SNP25 MOUSE STANDARD; PRT; 206 AA.
 AC P60879; P13795; P36974; P70557; Q81XK3; Q96FW2; Q9BR45;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
 25 kDa protein) (Super protein) (SUP).
 DE Names=Snap25; Synonyms=Snap;
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN NUCLEOTIDE SEQUENCE (ISOFORM SNAP-25A).
 RC STRAIN=BALB/c;
 RX MEDLINE=90078337; PubMed=2592413; DOI=10.1083/jcb.109.6.3039;
 RA Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,
 Bloom P.E., Wilson M.C.;
 RT "The identification of a novel synaptosomal-associated protein, SNAP-
 25, differentially expressed by neuronal subpopulations.";
 RL J. Cell Biol. 109:3039-3052(1989).
 [2]
 RN NUCLEOTIDE SEQUENCE (ISOFORM SNAP-25B).
 RC STRAIN=ILS, and ISS;
 RX MEDLINE=22347237; PubMed=12459461; DOI=10.1016/S0014-5793(02)03629-3;
 RA Hepp R., Cabanols J.P., Roche P.A.;
 RT "Differential phosphorylation of SNAP-25 in vivo by protein kinase C
 and protein kinase A.";
 RL FEBS Lett. 532:52-56(2002).
 CC -I- FUNCTION: t-SNARE involved in the molecular regulation of
 CC neurotransmitter release. May play an important role in the
 CC synaptic function of specific neuronal systems. Associates with
 CC proteins involved in vesicle docking and membrane fusion.
 CC -I- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
 CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
 CC SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with
 CC STX1A and VAMP8 (By similarity).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Isoforms differ by the usage of two alternative
 CC homologous exons (5a and 5b) which encode for positions 56 to 94
 CC and differ only in 9 positions out of 39;
 CC Name=SNAP-25b;
 CC IsoId=P60879-1, P13795-1;
 CC Sequences=Displayed;
 CC Name=SNAP-25a;
 CC IsoId=P60879-2, P13795-2;
 CC Sequence=VSP_010019;
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [4]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25A).
 RC STRAIN=C57BL/6; TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [5]
 RN INTERACTION WITH SNAP25BP.
 RX PubMed=10195194; DOI=10.1038/5673;
 RA Ilardi J.M., Mochida S., Sheng Z.-H.;
 RT "Snapin: a SNARE-associated protein implicated in synaptic
 RT transmission.";
 RL Nat. Neurosci. 2:119-124(1999).
 [6]
 RN PHOSPHORYLATION SITES THR-138 AND SER-187.
 RX MEDLINE=22347237; PubMed=12459461; DOI=10.1016/S0014-5793(02)03629-3;
 RA Hepp R., Cabanols J.P., Roche P.A.;
 RT "Differential phosphorylation of SNAP-25 in vivo by protein kinase C
 RT and protein kinase A.";
 RL FEBS Lett. 532:52-56(2002).
 CC -I- FUNCTION: t-SNARE involved in the molecular regulation of
 CC neurotransmitter release. May play an important role in the
 CC synaptic function of specific neuronal systems. Associates with
 CC proteins involved in vesicle docking and membrane fusion.
 CC -I- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
 CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
 CC SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with
 CC STX1A and VAMP8 (By similarity).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Isoforms differ by the usage of two alternative
 CC homologous exons (5a and 5b) which encode for positions 56 to 94
 CC and differ only in 9 positions out of 39;
 CC Name=SNAP-25b;
 CC IsoId=P60879-1, P13795-1;
 CC Sequences=Displayed;
 CC Name=SNAP-25a;
 CC IsoId=P60879-2, P13795-2;
 CC Sequence=VSP_010019;

CC -!- PTM: Palmitoylated (By similarity).
 CC -!- SIMILARITY: Belongs to the SNAP-25 family.
 CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; M22012; AAA61741.1; -; mRNA.
 CC EMBL; AF483516; AAL90790.1; -; mRNA.
 CC EMBL; AF483517; AAL90791.1; -; mRNA.
 CC EMBL; AK078038; BAC37105.1; -; mRNA.
 CC EMBL; BC018249; AAL18249.1; -; mRNA.
 CC PIR; A33623; A33623.
 CC PDB; 2BU0; Model; C=18-82, D=139-206.
 CC SMR; P60879; 7-83, 131-204.
 CC Ensembl; ENSMUSG00000027273; Mus musculus.
 CC MGI; MGI.98331; Snap25.
 CC GO; GO:0005886; C:plasma membrane; TAS.
 CC GO; GO:0000149; F:SNARE binding; IDA.
 CC GO; GO:0007269; P:neurotransmitter secretion; IMP.
 CC InterPro; IPR000928; SNAP-25.
 CC InterPro; IPR000727; T-SNARE.
 CC Pfam; PF00835; SNAP-25; 1.
 CC Pfam; PF05739; SNARE; 1.
 CC SMART; SM00397; t-SNARE; 2.
 CC PROSITE; PS50192; T-SNARE; 2.
 CC 3D-structure; Alternative splicing; Coiled coil; Lipoprotein;
 CC Palmitate; Phosphorylation; Repeat; Synaptosome.
 CC DOMAIN 19 81 t-SNARE coiled-coil homology 1.
 CC DOMAIN 140 202 t-SNARE coiled-coil homology 2.
 CC Cys-rich.
 CC SITE 85 92 Cleavage (by BONT/E) (By similarity).
 CC SITE 180 181 Phosphothreonine (by PKC and PKA).
 CC MOD_RES 138 138 Phosphoserine (by PKC).
 CC MOD_RES 187 187 Phosphoserine (by PKC).
 CC VARSPIC 58 89 ERIEGMDQINKMKAEKNTDLGKFCGLCV -> DRVVEE
 CC GNNHINQDMKEAKNLDLGGKCCGLFI (in isoform
 CC SNAP-25a).
 CC /FTId=VSP_010019.
 CC SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;

Query Match 100.0%; Score 84; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred.No. 7.4e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANORATKMLGSG 18
 |||||
 Db 190 TRIDEANORATKMLGSG 206

Search completed: April 3, 2006, 15:46:26
 Job time : 98.9633 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:30:10 ; Search time 10.2844 Seconds
(without alignments)
177.756 Million cell updates/sec

Title: US-09-942-098-92
Perfect score: 84
Sequence: 1 XTRIDEANQRATKMLGSGX 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*

1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	203	2 I50481	synapse protein SN
2	84	100.0	204	2 I50480	synapse protein SN
3	84	100.0	206	2 A37861	synaptosomal-assoc
4	84	100.0	206	2 I53735	nerve terminal pro
5	84	100.0	206	2 I67823	nerve terminal pro
6	84	100.0	206	2 A33623	synaptosomal-assoc
7	54	64.3	210	2 I50552	synapse protein -
8	48	57.1	29	2 A49708	synaptosomal-assoc
9	46	54.8	1361	2 A29959	DNA-directed RNA p
10	45	53.6	296	2 D87525	conserved hypothe
11	44	52.4	278	2 AH3356	comE operon protei
12	44	52.4	1578	2 S76238	hypothetical prote
13	42	50.0	83	2 A33854	outer membrane lip
14	42	50.0	1056	2 T33167	hypothetical prote
15	41	48.8	158	2 JC5297	vesicle-membrane f
16	41	48.8	210	2 JC5512	SNARE protein 23 -
17	41	48.8	211	2 JC5296	vesicle-membrane f
18	41	48.8	542	2 T23869	hypothetical prote
19	41	48.8	602	2 T29386	hypothetical prote
20	41	48.8	2288	2 T29399	hypothetical prote
21	40	47.6	260	2 S77848	probable valine-tr
22	40	47.6	408	2 A2473	hypothetical prote
23	40	47.6	490	2 G71563	hypothetical prote
24	40	47.6	540	2 T34187	hypothetical prote
25	40	47.6	609	2 T52524	hypothetical prote
26	40	47.6	642	2 G90551	lipoprotein [impor
27	40	47.6	740	2 G75477	probable general s
28	39	46.4	91	2 A69282	hypothetical prote
29	39	46.4	241	1 RRNZ	phosphoprotein P -

30	39	46.4	241	1 RRNZPP	phosphoprotein P -
31	39	46.4	296	2 A82325	rod shape-determin
32	39	46.4	345	2 H83854	NAD(P)H-dependent
33	39	46.4	552	2 C87259	lysyl-tRNA synthet
34	39	46.4	577	1 G46328	hemagglutinin-neur
35	39	46.4	577	1 D46328	hemagglutinin-neur
36	39	46.4	577	1 E46328	hemagglutinin-neur
37	39	46.4	577	1 F46328	hemagglutinin-neur
38	39	46.4	577	1 HNZNC	hemagglutinin-neur
39	39	46.4	602	2 T48697	hypothetical prote
40	39	46.4	704	2 S25586	lcrD protein - Yer
41	39	46.4	1198	2 T34340	dynein heavy chain
42	39	46.4	2427	2 T16613	hypothetical prote
43	39	46.4	3033	1 JQ1303	genome polyprotein
44	38.5	45.8	461	2 T35151	hypothetical prote
45	38.5	45.8	1196	2 H85061	hypothetical prote

ALIGNMENTS

RESULT 1

I50481
synapse protein SNAP-25 - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50481
R;Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Accession: I50481
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-203 <RIS>
A;Cross-references: UNIPROT:P36978; UNIPARC:UPI0000135B03; GB:L22976; NID:G349430; PIDN:?
C;Genetics:
A;Gene: SNAP-25

Query Match 100.0%; Score 84; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
Db 187 TRIDEANQRATKMLGSG 203
|||||

RESULT 2

I50480
synapse protein SNAP-25 - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50480
R;Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Accession: I50480
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-204 <RIS>
A;Cross-references: UNIPROT:P36977; UNIPARC:UPI0000135B02; GB:L22973; NID:G349426; PIDN:?
C;Genetics:
A;Gene: SNAP-25

Query Match 100.0%; Score 84; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TRIDEANQRATKMLGSG 18
Db 188 TRIDEANQRATKMLGSG 204
|||||

```
RESULT 3
A37861
synaptosomal-associated 25K protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
C;Accession: A37861
R;Catsicas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coincides with the expression of a novel synaptosomal-associated protein, SNAP-25, in differentiating retinal ganglion cells.
A;Reference number: A37861; MUID:91126080; PMID:1992470
A;Accession: A37861
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <CAT>
A;Cross-references: UNIPROT:P60878; UNIPARC:UPI0000001103; GB:M57957; NID:g212673; PIDN:
A;Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 84; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
|||||
Db 190 TRIDEANQRATKMLGSG 206

RESULT 4
I53735
nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I53735
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein SNAP-25.
A;Reference number: I53735; MUID:94156217; PMID:8112622
A;Accession: I53735
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: UNIPROT:P60880; UNIPARC:UPI000002B3DD; GB:L19760; NID:g307425; PIDN:
C;Genetics:
A;Gene: GDB:SNAP
A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 84; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
|||||
Db 190 TRIDEANQRATKMLGSG 206

RESULT 5
I67823
nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I67823
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein SNAP-25.
A;Reference number: I53735; MUID:94156217; PMID:8112622
A;Accession: I67823
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: UNIPROT:P60880; UNIPARC:UPI0000001103; GB:L19761; NID:g307427; PIDN:
A;Genetics:
A;Gene: GDB:SNAP
```

```
A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 84; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
|||||
Db 190 TRIDEANQRATKMLGSG 206

RESULT 6
A33623
synaptosomal-associated 25K protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 09-Jul-2004
C;Accession: A33623
R;Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.; J. Cell Biol. 109, 3039-3052, 1989
A;Title: The identification of a novel synaptosomal-associated protein, SNAP-25, in differentiating retinal ganglion cells.
A;Reference number: A33623; MUID:90078337; PMID:2592413
A;Accession: A33623
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <OYL>
A;Cross-references: UNIPROT:P60879; UNIPARC:UPI0000001103; GB:M22012; GB:X51673; NID:g201103

Query Match 100.0%; Score 84; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
|||||
Db 190 TRIDEANQRATKMLGSG 206

RESULT 7
I50552
synapse protein - marbled electric ray
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50552
R;Risinger, C.; Blomqvist, A.G.; Lundell, I.; Lambertsson, A.; Nassef, D.; Pieribone, V.F. J. Biol. Chem. 268, 24408-24414, 1993
A;Title: Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25) in differentiating retinal ganglion cells.
A;Reference number: A49513; MUID:94043281; PMID:8226991
A;Accession: I50552
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-210 <RIS>
A;Cross-references: UNIPROT:P36976; UNIPARC:UPI0000135AFB; GB:L22020; NID:g431296; PIDN:

Query Match 64.3%; Score 54; DB 2; Length 210;
Best Local Similarity 84.6%; Pred. No. 0.057;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RIDEANQRATKML 15
|||||
Db 198 RIDEANQRATKML 210

RESULT 8
A49708
synaptosomal-associated 25K protein - rat (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 12-Jun-1998
C;Accession: A49708
R;Binz, T.; Biasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.; J. Biol. Chem. 269, 1617-1620, 1994
A;Title: Proteolysis of SNAP-25 by types E and A botulin neurotoxins.
A;Reference number: A49708; MUID:94124495; PMID:8294407
A;Accession: A49708
```

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-29 <BIN>
A;Cross-references: UNIPARC:UPI000017C9D4

Query Match 57.1%; Score 48; DB 2; Length 29;
Best Local Similarity 62.5%; Pred. No. 0.077;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 RIDEANORATKMLGSG 18
:|:|||||
Db 14 KADSNKTRATKMLGSG 29

RESULT 9
A29959
DNA-directed RNA polymerase (EC 2.7.7.6) beta'' chain - spinach chloroplast
C;Species: chloroplast Spinacia oleracea (spinach)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29959
R;Hudson, G.S.; Holton, T.A.; Whitfield, P.R.; Bottomley, W.
J. Mol. Biol. 200, 639-654, 1988
A;Title: Spinach chloroplast rpoBC genes encode three subunits of the chloroplast RNA polymerase
A;Reference number: A29959; MUID:88316931; PMID:3045324
A;Accession: A29959
A;Molecule type: DNA
A;Residues: 1-1361 <HUD>
A;Cross-references: UNIPROT:P11704; UNIPARC:UPI0000134774; EMBL:M55297; NID:g295119; PID:11704
C;Genetics:
A;Gene: rpoC-2
A;Genome: chloroplast
C;Superfamily: chloroplast DNA-directed RNA polymerase beta''-2 chain
C;Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 54.8%; Score 46; DB 2; Length 1361;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RIDEANORATKMLGS 17
||| |:|||
Db 1156 RIDSWNERITRLGS 1170

RESULT 10
D87525
conserved hypothetical protein CC2229 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D87525
R;Niernman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonin, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87525
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-296 <STO>
A;Cross-references: UNIPROT:Q9A665; UNIPARC:UPI00000C765E; GB:AE005673; NID:g13423736; F:Q9A665
C;Genetics:
A;Gene: CC2229

Query Match 53.6%; Score 45; DB 2; Length 296;
Best Local Similarity 60.0%; Pred. No. 3.4;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 IDEANORATKMLGSG 18
:|:|||||
Db 250 VDWANQLTKLAGSG 264

RESULT 11

AH3356
comE operon protein 3 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AH3356
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.; Mavur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessac, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688
A;Accession: AH3356
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-278 <KUR>
A;Cross-references: UNIPROT:Q8YHG3; UNIPARC:UPI0000057E30; GB:AE008917; PIDN:AAL52019.1;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI0838
A;Map position: 1

Query Match 52.4%; Score 44; DB 2; Length 278;
Best Local Similarity 69.2%; Pred. No. 4.8;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 EANORATKMLGSG 18
|:|||||
Db 146 ETERRATPMLGSG 158

RESULT 12
S76238
hypothetical protein sll0267 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76238
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76238
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1578 <KAN>
A;Cross-references: UNIPROT:P74400; UNIPARC:UPI00000C10E9; EMBL:D90914; GB:AB001339; NID:1578
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 52.4%; Score 44; DB 2; Length 1578;
Best Local Similarity 57.1%; Pred. No. 32;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RIDEANORATKMLG 16
:|:|||||
Db 1004 QLDQANORATKMLG 1017

RESULT 13
A33854
outer membrane lipoprotein I precursor - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 09-Jul-2004
C;Accession: A33854; S04834; A44834; A83288
R;Duchene, M.; Barron, C.; Schweizer, A.; von Specht, B.U.; Domdey, H. J. Bacteriol. 171, 4130-4137, 1989
A;Title: Pseudomonas aeruginosa outer membrane lipoprotein I gene: molecular cloning, sequence analysis, and expression
A;Reference number: A33854; MUID:89327122; PMID:2502533
A;Accession: A33854
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <DUC>
A;Cross-references: UNIPROT:P11221; UNIPARC:UPI000002C273; GB:M25761; NID:g151334; PIDN:P11221

R;Cornelis, P.; Bouia, A.; Belarbi, A.; Guyonvarch, A.; Kammerer, B.; Hannaert, V.; Hube Mol. Microbiol. 3, 421-428, 1989
A;Title: Cloning and analysis of the gene for the major outer membrane lipoprotein from A;Reference number: S04834; MUID:89313294; PMID:2473376
A;Accession: S04834
A;Molecule type: DNA
A;Residues: 1-83 <COR>
A;Cross-references: UNIPARC:UPI000002C273; EMBL:X13748; NID:g45344; PIDN:CAA32013.1; PIDN:CAA32013.1; PIDN:CAA32013.1; PIDN:CAA32013.1
A;Note: the authors translated the codon GAA for residue 78 as Gly
R;Saint-Onge, A.; Romeyer, F.; Lebel, P.; Masson, L.; Brousseau, R.
J. Gen. Microbiol. 138, 733-741, 1992
A;Title: Specificity of the Pseudomonas aeruginosa PA01 lipoprotein I gene as a DNA probe
A;Reference number: A44834; MUID:92268853; PMID:1588307
A;Accession: A44834
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <SAI>
A;Cross-references: UNIPARC:UPI000002C273; GB:X58714; GB:S36066; NID:g433509; PIDN:CAA41
A;Experimental source: PA01
A;Note: sequence extracted from NCBI backbone (NCBI:103666, NCBIP:103667)
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A82950
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-83 <STO>
A;Cross-references: UNIPARC:UPI000002C273; GB:AE004712; GB:AE004091; NID:g9948940; PIDN:AE004091
A;Experimental source: strain PA01
C;Genetics:
A;Gene: oprI; PA2853
C;Keywords: lipid binding; lipoprotein; membrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-83/Product: lipoprotein I #status predicted <MAT>
Query Match 50.0%; Score 42; DB 2; Length 83;
Best Local Similarity 72.7%; Pred. No. 2.9;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 5 DEANORATKML 15
Db 67 DEANERAIKML 77
RESULT 14
T33167
hypothetical protein T26C12.4 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33167; D88645
R;Gattung, S.; Scheet, P.; Harper, M.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid T26C12.
A;Reference number: Z21296
A;Accession: T33167
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1056 <GAT>
A;Cross-references: UNIPROT:O61859; UNIPARC:UPI0000176113; EMBL:AF067623; PIDN:AAC17555.
A;Experimental source: strain Bristol N2; Clone T26C12
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.elegans/ for the complete genome sequence
A;Accession: D88645
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1056 <STO>

A;Cross-references: UNIPARC:UPI0000176113; GB:chr_IV; PIDN:AAC17555.1; PID:g3158511; GSPF C;Genetics:
A;Gene: CESP.T26C12.4
A;Map position: 4
A;Introns: 41/2; 197/1; 263/3; 294/3; 793/2; 865/2; 904/3
C;Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain homol
Query Match 50.0%; Score 42; DB 2; Length 1056;
Best Local Similarity 61.5%; Pred. No. 47;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 4 IDEANORATKMLG 16
Db 823 LEEANVRADKLLG 835
RESULT 15
JC5297
vesicle-membrane fusion protein SNAP-23B - human
C;Species: Homo sapiens (man)
C;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: JC5297
R;Mollinedo, F.; Lazo, P.A.
Biochem. Biophys. Res. Commun. 231, 808-812, 1997
A;Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23 in rat brain
A;Reference number: JC5296; MUID:97224437; PMID:9070898
A;Accession: JC5297
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-158 <MOL>
A;Cross-references: UNIPROT:Q00161; UNIPARC:UPI000002B3DC; GB:Y09568; NID:g1924943; PIDN:Q00161
A;Experimental source: neurophils
C;Comment: This protein is involved in regulating exocytosis in human neurophils, a cent
Query Match 48.8%; Score 41; DB 2; Length 158;
Best Local Similarity 60.0%; Pred. No. 8.8;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 3 RIDEANORATKMLGS 17
Db 144 RIDIANARAKKLIDS 158
Search completed: April 3, 2006, 15:31:25
Job time : 11.2844 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:27:08 ; Search time 97.4404 Seconds
(without alignments)
85.675 Million cell updates/sec

Title: US-09-942-098-92

Perfect score: 84

Sequence: 1 XTRIDEANQRATKWLGSX 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1980s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100.0	19	6 AAE36740	Aae36740 Fret subs
2	84	100.0	19	6 AAE36737	Aae36737 Fret subs
3	84	100.0	19	7 ABW01793	Abw01793 FRET subs
4	84	100.0	19	7 ABW01796	Abw01796 FRET subs
5	84	100.0	20	2 AAW30100	Aaw30100 Neurotran
6	84	100.0	22	6 AAE36738	Aae36738 Fret subs
7	84	100.0	22	6 ABW01794	Abw01794 FRET subs
8	84	100.0	23	6 AAE36733	Aae36733 Fret subs
9	84	100.0	23	7 ABW01789	Abw01789 FRET subs
10	84	100.0	24	6 AAE36735	Aae36735 Fret subs
11	84	100.0	24	7 ABW01791	Abw01791 FRET subs
12	84	100.0	26	2 AAW30099	Aaw30099 Neurotran
13	84	100.0	33	6 AAE36682	Aae36682 Goldfish
14	84	100.0	33	6 AAE36678	Aae36678 Goldfish
15	84	100.0	33	6 ABW01739	Abw01739 Goldfish
16	84	100.0	33	7 ABW01734	Abw01734 Mouse SNA
17	84	100.0	33	7 ABW01738	Abw01738 Goldfish
18	84	100.0	33	8 ADM97054	Adm97054 Botulinum
19	84	100.0	33	8 ADM97053	Adm97053 Botulinum
20	84	100.0	33	8 ADM97049	Adm97049 Botulinum
21	84	100.0	33	9 AEA14927	Aea14927 Goldfish
22	84	100.0	33	9 AEA14923	Aea14923 SNAP-25 s
23	84	100.0	33	9 AEA14928	Aea14928 Goldfish
24	84	100.0	33	9 AEA14928	Aea14928 Goldfish

ALIGNMENTS

RESULT 1

AAE36740

ID AAE36740 standard; peptide; 19 AA.

XX AC AAE36740;

XX AC AAE36740;

DT 07-AUG-2003 (first entry)

DE Fret substrate peptide #11 used in the invention.

XX Clostridium toxin; protease activity; botulinum toxin; BONT; TeNT;

KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;

KW cosmetic.

XX Unidentified.

OS Unidentified.

XX Key

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is fret
 CC substrate peptide used in the exemplification of the invention
 XX
 SQ Sequence 19 AA;

Query Match 100.0%; Score 84; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKMLGSG 18
 |||||
 DB 2 TRIDEANORATKMLGSG 18

RESULT 2
 AAEE36737
 ID AAEE36737 standard; peptide; 19 AA.
 XX
 AC AAEE36737;

DT 07-AUG-2003 (first entry)

DE Fret substrate peptide #8 used in the invention.

XX Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW cosmetic.

XX Unidentified.

XX Key Location/Qualifiers
 FH Modified-site 1 /note= "Fluorescein-modified Lysine; This residue is
 FT given as Xaa in the sequence shown as SEQ ID NO: 92 in
 FT the sequence listing of the specification"
 FT Modified-site 19
 FT /note= "Tetramethylrhodamine-modified Lysine; C-terminal
 FT amide; This residue is given as Xaa in the sequence shown
 FT as SEQ ID NO: 92 in the sequence listing of the
 FT specification"

XX WO2003020948-A2.

XX 13-MAR-2003.

XX 22-AUG-2002; 2002WO-US027145.

XX 28-AUG-2001; 2001US-00942024.

XX (ALLR) ALLERGAN INC.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-290198/28.

XX Botulinum serotype A/E substrate useful for assaying protease activity of

PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 PT toxin recognition sequence that includes a cleavage site.
 XX
 PS Example 1; Page 115; 168pp; English.

XX The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is fret
 CC substrate peptide used in the exemplification of the invention
 XX
 SQ Sequence 19 AA;

Query Match 100.0%; Score 84; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKMLGSG 18
 |||||
 DB 2 TRIDEANORATKMLGSG 18

RESULT 3
 ABW01793
 ID ABW01793 standard; peptide; 19 AA.
 XX
 AC ABW01793;

DT 12-FEB-2004 (first entry)

DE FRET substrate #6 to analyse proteolytic activity of botulinum toxin.

XX Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
 KW FRET; fluorescence resonance energy transfer.

XX Unidentified.

XX Key Location/Qualifiers
 FH Modified-site 1 /note= "Fluoresceinated lysine"
 FT Modified-site 19
 FT /note= "Tetramethylrhodamine labelled lysine; C-terminal
 FT amide"

XX US2003143651-A1.

XX 31-JUL-2003.

XX 28-AUG-2001; 2001US-00942098.

XX 28-AUG-2001; 2001US-00942098.

XX (STEW/) STEWARD L E.

XX (FERN/) FERNANDEZ-SALAS E.

XX (AOKI/) AOKI K R.

XX Steward LE, Fernandez-Salas E, Aoki KR;

DR WPI; 2003-829791/77.
 XX Determining clostridial toxin protease activity, by treating sample with
 PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
 PT sequence, under conditions which exhibit resonance energy transfer.
 XX
 XX Example 1; Page 29; Opp; English.
 XX
 CC The present invention provides clostridial toxin substrates useful in
 CC assaying for the protease activity of any clostridial toxin including
 CC toxins of all serotypes as well as tetanus toxins. The present sequence
 CC is FRET (fluorescence resonance energy transfer) substrate to analyse
 CC proteolytic activity of botulinum toxin. This substrate is used in the
 CC exemplification of the invention
 XX
 XX Sequence 19 AA;
 Query Match 100.0%; Score 84; DB 7; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TRIDEANQRATKMLGSG 18
 |||||
 Db 2 TRIDEANQRATKMLGSG 18
 |||||
 RESULT 4
 AEW01796
 ID AEW01796 standard; peptide; 19 AA.
 AC AEW01796;
 XX
 XX 12-FEB-2004 (first entry)
 DE FRET substrate #9 to analyse proteolytic activity of botulinum toxin.
 XX Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
 KW FRET; fluorescence resonance energy transfer.
 XX
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "DABCYL labelled lysine"
 FT Modified-site 19 /note= "EDANS labelled lysine; C-terminal amide"
 FT US2003143651-A1.
 PN
 XX 31-JUL-2003.
 PD
 XX 28-AUG-2001; 2001US-00942098.
 PF
 XX 28-AUG-2001; 2001US-00942098.
 PR
 XX (STEW/) STEWARD L E.
 PA (FERN/) FERNANDEZ-SALAS E.
 PA (AOKI/) AOKI K R.
 XX
 XX Steward LE, Fernandez-Salas E, Aoki KR;
 PI
 XX WPI; 2003-829791/77.
 DR
 XX Determining clostridial toxin protease activity, by treating sample with
 PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
 PT sequence, under conditions which exhibit resonance energy transfer.
 XX
 XX Example 1; Page 29; Opp; English.
 PS
 CC The present invention provides clostridial toxin substrates useful in
 CC assaying for the protease activity of any clostridial toxin including
 CC toxins of all serotypes as well as tetanus toxins. The present sequence
 CC is FRET (fluorescence resonance energy transfer) substrate to analyse

CC proteolytic activity of botulinum toxin. This substrate is used in the
 CC exemplification of the invention
 XX
 XX Sequence 19 AA;
 Query Match 100.0%; Score 84; DB 7; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TRIDEANQRATKMLGSG 18
 |||||
 Db 2 TRIDEANQRATKMLGSG 18
 |||||
 RESULT 5
 AAW30100
 ID AAW30100 standard; peptide; 20 AA.
 XX
 AC AAW30100;
 XX
 XX 06-APR-1998 (first entry)
 DT
 XX Neurotransmitter secretion inhibitor #4.
 DE
 XX Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
 KW excitation-secretory uncoupling peptide; catecholamine secretion;
 KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
 KW synaptosomal associated protein; SNAP-25.
 XX
 OS Homo sapiens.
 XX
 XX WO9734620-A1.
 PN
 XX 25-SEP-1997.
 PD
 XX 18-MAR-1997; 97WO-US004393.
 PF
 XX 18-MAR-1996; 96US-0013599P.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Montal M;
 PI
 XX WPI; 1997-479986/44.
 DR
 XX Excitation-secretory uncoupling peptide(s) for inhibiting
 PT neurotransmitter release - used particularly for treating muscle
 PT spasticity, and for delivering drugs specifically to neural cells.
 PT
 XX Claim 14; Page 32; 61pp; English.
 PS
 XX This sequence corresponds to residues 187-206 of the human 25 kD
 CC synaptosomal associated protein (SNAP-25), and is a inhibitory agent of
 CC the invention. The agents of the invention inhibit secretion of
 CC neurotransmitter from neuronal cells and is an excitation-secretory
 CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which
 CC correspond substantially to any one of AAW30097-W30102, or more generally
 CC any (I) that inhibits 50% of catecholamine secretion from bovine
 CC chromaffin cells at a concentration of 10 microm, especially 0.25 microm,
 CC or less. (I) are used, as a replacement for Clostridium toxin, to inhibit
 CC release of neurotransmitters from synaptic vesicles, specifically for
 CC reducing muscle spasticity. Also (I) may be labelled to allow in vivo
 CC imaging of intracellular distribution of (I). Compounds for delivering
 CC the drug to neural cells provide targeted drug delivery, e.g. of
 CC substance P to brain tumours for induction of apoptosis. Unlike the
 CC neurotoxins, (I) are not toxic or immunogenic and are more readily
 CC available. Their therapeutic effect lasts for several days or weeks, so
 CC lower doses or less frequent treatments are required
 XX
 XX Sequence 20 AA;
 Query Match 100.0%; Score 84; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
Db 4 TRIDEANQRATKMLGSG 20
|||||

RESULT 6
AAE36738
ID AAE36738 standard; peptide; 22 AA.
XX
AC AAE36738;
XX
DT 07-AUG-2003 (first entry)
XX
DE Fret substrate peptide #9 used in the invention.
XX
KW Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
KW cosmetic.
XX Unidentified.

OS XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Fluorescein-modified Lysine; This residue is
FT given as Xaa in the sequence shown as SEQ ID NO: 93 in
FT the sequence listing of the specification"
FT Modified-site 22
FT /note= "Tetramethylrhodamine-modified Lysine; C-terminal
FT amide; This residue is given as Xaa in the sequence shown
FT as SEQ ID NO: 93 in the sequence listing of the
FT specification"
XX
PN WO2003020948-A2.
XX
XX 13-MAR-2003.
XX
XX 22-AUG-2002; 2002WO-US027145.
XX
XX 28-AUG-2001; 2001US-00942024.
XX
XX (ALLR) ALLERGAN INC.
XX
XX Steward LE, Fernandez-Salas E, Aoki KR;
XX WPI; 2003-290198/28.
XX
XX Botulinum serotype A/E substrate useful for assaying protease activity of
XX botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
XX toxin recognition sequence that includes a cleavage site.
XX
XX Example 1; Page 115; 168pp; English.

CC The present invention relates to novel clostridium toxin substrates. The
CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
CC which comprise a donor fluorophore, an acceptor having an absorbance
CC spectrum overlapping the emission spectrum of the donor fluorophore and a
CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
CC the cleavage site intervenes between the donor fluorophore and acceptor
CC and under the appropriate conditions, the resonance energy transfer is
CC exhibited between the donor and acceptor. Natural targets of clostridium
CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
CC of the invention are useful in assaying for the protease activity of any
CC clostridial toxin including botulinum toxins of all serotypes and tetanus
CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
CC samples, water samples, cosmetics, tissue samples and beverage or food
CC samples. They are useful to assay a sample from a human or animal, for
CC e.g., exposed to clostridial toxin or having one or more symptoms of a
CC clostridial toxin, to follow activity during production and purification
CC of clostridial toxin and to assay formulated clostridial toxin products
CC including pharmaceuticals and cosmetics. The present sequence is fret

CC substrate peptide used in the exemplification of the invention
XX
SQ Sequence 22 AA;
Query Match 100.0%; Score 84; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
Db 5 TRIDEANQRATKMLGSG 21
|||||

RESULT 7
ABW01794
ID ABW01794 standard; peptide; 22 AA.
XX
AC ABW01794;
XX
DT 12-FEB-2004 (first entry)
XX
DE FRET substrate #7 to analyse proteolytic activity of botulinum toxin.
XX
KW Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
KW FRET; fluorescence resonance energy transfer.
XX Unidentified.

OS XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Fluoresceinated lysine"
FT Modified-site 22 /note= "Tetramethylrhodamine labelled lysine; C-terminal
FT amide"
XX
PN US2003143651-A1.
XX
XX 31-JUL-2003.
XX
XX 28-AUG-2001; 2001US-00942098.
XX
XX 28-AUG-2001; 2001US-00942098.
XX (STEW/) STEWARD L E.
XX (PERN/) FERNANDEZ-SALAS E.
XX (AOKI/) AOKI K R.
XX
XX Steward LE, Fernandez-Salas E, Aoki KR;
XX WPI; 2003-829791/77.
XX
XX Determining clostridial toxin protease activity, by treating sample with
XX clostridial substrate with donor fluorophore, acceptor, toxin recognition
XX sequence, under conditions which exhibit resonance energy transfer.
XX
XX Example 1; Page 29; Opp; English.

CC The present invention provides clostridial toxin substrates useful in
CC assaying for the protease activity of any clostridial toxin including
CC toxins of all serotypes as well as tetanus toxins. The present sequence
CC is FRET (fluorescence resonance energy transfer) substrate to analyse
CC proteolytic activity of botulinum toxin. This substrate is used in the
CC exemplification of the invention
XX
SQ Sequence 22 AA;
Query Match 100.0%; Score 84; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
Db 5 TRIDEANQRATKMLGSG 21
|||||

RESULT 8
AAE36733
ID AAE36733 standard; peptide; 23 AA.

AC AAE36733;

XX 07-AUG-2003 (first entry)

DT Fret substrate peptide #4 used in the invention.

DE Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;

XX tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;

XX cosmetic.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Fluorescein-modified Lysine; This residue is given as Xaa in the sequence shown as SEQ ID NO: 88 in the sequence listing of the specification"

FT Modified-site 23 /note= "Tetramethylrhodamine-modified Lysine; C-terminal amide; This residue is given as Xaa in the sequence shown as SEQ ID NO: 88 in the sequence listing of the specification"

XX WO2003020948-A2.

XX 13-MAR-2003.

XX 22-AUG-2002; 2002WO-US027145.

XX 28-AUG-2001; 2001US-00942024.

XX (ALLR) ALLERGAN INC.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-290198/28.

XX Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.

XX Example 1; Page 115; 168pp; English.

XX The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/E (BoNT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a BoNT A or BoNT/E recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus toxins (TeNT) in a sample including bacterial, baculoviral and yeast lysate, raw, cooked or processed foods, beverages, animal feed, soil samples, water samples, cosmetics, tissue samples and beverage or food samples. They are useful to assay a sample from a human or animal, for e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is fret substrate peptide used in the exemplification of the invention

XX Sequence 23 AA;

XX Query Match 100.0%; Score 84; DB 6; Length 23;

Best Local Similarity 100.0%; Pred. No. 2e-07; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 2 TRIDEANQRATKMLGSG 18

DB 6 TRIDEANQRATKMLGSG 22

RESULT 9

ABW01789

ID ABW01789 standard; peptide; 23 AA.

XX ABW01789;

DT 12-FEB-2004 (first entry)

XX FRET substrate #2 to analyse proteolytic activity of botulinum toxin.

XX Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;

KW FRET; fluorescence resonance energy transfer.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Fluoresceinated lysine"

FT Modified-site 23 /note= "Tetramethylrhodamine labelled lysine; C-terminal amide"

XX US2003143651-A1.

XX 31-JUL-2003.

XX 28-AUG-2001; 2001US-00942098.

XX 28-AUG-2001; 2001US-00942098.

XX (STEW/) STEWARD L E.

XX (PERN/) FERNANDEZ-SALAS E.

XX (AOKI/) AOKI K R.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-829791/77.

XX Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.

XX Example 1; Page 29; Opp; English.

XX The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is FRET (fluorescence resonance energy transfer) substrate to analyse proteolytic activity of botulinum toxin. This substrate is used in the exemplification of the invention

XX Sequence 23 AA;

XX Query Match 100.0%; Score 84; DB 7; Length 23;

XX Best Local Similarity 100.0%; Pred. No. 2e-07;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18

DB 6 TRIDEANQRATKMLGSG 22

RESULT 10

AAE36735

ID AAE36735 standard; peptide; 24 AA.

DE Neurotransmitter secretion inhibitor #3.

XX Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;

KW excitation-secretory uncoupling peptide; catecholamine secretion;

KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;

KW synaptosomal associated protein; SNAP-25.

OS Homo sapiens.

XX WO9734620-A1.

PN 25-SEP-1997.

XX 18-MAR-1997; 97WO-US004393.

XX 18-MAR-1996; 96US-0013599P.

XX (REGC) UNIV CALIFORNIA.

PA Montal M;

XX WPI; 1997-479986/44.

DR Excitation-secretory uncoupling peptide(s) for inhibiting

XX neuro-transmitter release - used particularly for treating muscle

PT spasticity, and for delivering drugs specifically to neural cells.

PT Claim 13; Page 31; 61pp; English.

PS This sequence corresponds to residues 181-206 of the human 25 kD

XX synaptosomal associated protein (SNAP-25), and is an inhibitory agent of

CC the invention. The agents of the invention inhibit secretion of

CC neurotransmitter from neuronal cells and is an excitation-secretory

CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which

CC correspond substantially to any one of AAW30097-W30102, or more generally

CC any (I) that inhibits 50% of catecholamine secretion from bovine

CC chromaffin cells at a concentration of 10 microm, especially 0.25 microm,

CC or less. (I) are used, as a replacement for Clostridium toxin, to inhibit

CC release of neurotransmitters from synaptic vesicles, specifically for

CC reducing muscle spasticity. Also (I) may be labelled to allow in vivo

CC imaging of intracellular distribution of (I). Compounds for delivering

CC the drug to neural cells provide targeted drug delivery, e.g. of

CC substance P to brain tumours for induction of apoptosis. Unlike the

CC neurotoxins, (I) are not toxic or immunogenic and are more readily

CC available. Their therapeutic effect lasts for several days or weeks, so

CC lower doses or less frequent treatments are required

XX Sequence 26 AA;

SQ Query Match 100.0%; Score 84; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. NO. 2.3e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKMLGSG 18

Db 10 TRIDEANORATKMLGSG 26

RESULT 13

AAE36682

ID AAE36682 standard; peptide; 33 AA.

AC AAE36682;

XX 07-AUG-2003 (first entry)

XX Goldfish SNAP-25A peptide.

XX Goldfish; clostridium toxin; protease activity; botulinum toxin; BONT;

KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;

KW TeNT; cosmetic.

XX Carassius auratus.

OS

XX Key Location/Qualifiers

FT Cleavage-site 7..8

FT /note= "BONT/E sensitive cleavage site"

FT Cleavage-site 24..25

FT /note= "BONT/A sensitive cleavage site"

FT Cleavage-site 25..26

FT /note= "BONT/C sensitive cleavage site"

XX WO2003020948-A2.

PN 13-MAR-2003.

XX 22-AUG-2002; 2002WO-US027145.

PF 28-AUG-2001; 2001US-00942024.

XX (ALLR) ALLERGAN INC.

XX Steward LE, Fernandez-Salas E, Aoki KR;

PI WPI; 2003-290198/28.

DR Botulinum serotype A/E substrate useful for assaying protease activity of

XX botulinum toxins, comprises donor fluorophore, acceptor and a clostridial

PT toxin recognition sequence that includes a cleavage site.

PT Disclosure; Page 42; 168pp; English.

PS The present invention relates to novel clostridium toxin substrates. The

XX invention further relates to botulinum serotype A/E (BONT/A/E) substrates

CC which comprise a donor fluorophore, an acceptor having an absorbance and a

CC spectrum overlapping the emission spectrum of the donor fluorophore and a

CC BONT A or BONT/E recognition sequence comprising a cleavage site, where

CC the cleavage site intervenes between the donor fluorophore and acceptor

CC and under the appropriate conditions, the resonance energy transfer is

CC exhibited between the donor and acceptor. Natural targets of clostridium

CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences

CC of the invention are useful in assaying for the protease activity of any

CC clostridial toxin including botulinum toxins of all serotypes and tetanus

CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast

CC lysate, raw, cooked or processed foods, beverages, animal feed, soil

CC samples, water samples, cosmetics, tissue samples and beverage or food

CC e.g., exposed to clostridial toxin or having one or more symptoms of a

CC clostridial toxin, to follow activity during production and purification

CC of clostridial toxin and to assay formulated clostridial toxin products

CC including pharmaceuticals and cosmetics. The present sequence is goldfish

CC SNAP-25A peptide used in the invention

XX Sequence 33 AA;

SQ Query Match 100.0%; Score 84; DB 6; Length 33;

Best Local Similarity 100.0%; Pred. NO. 3e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANORATKMLGSG 18

Db 17 TRIDEANORATKMLGSG 33

RESULT 14

AAE36683

ID AAE36683 standard; peptide; 33 AA.

XX AAE36683;

XX 07-AUG-2003 (first entry)

XX Goldfish SNAP-25B peptide.

XX Goldfish; clostridium toxin; protease activity; botulinum toxin; BONT;

XX tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;

KW

KW TeNT; cosmetic.
 XX
 KW Carassius auratus.
 OS
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 7. .8
 FT /note= "BoNT/E sensitive cleavage site"
 FT Cleavage-site 24. .25
 FT /note= "BoNT/A sensitive cleavage site"
 FT Cleavage-site 25. .26
 FT /note= "BoNT/C sensitive cleavage site"
 FT
 XX
 XX WO2003020948-A2.
 PN
 XX
 XX 13-MAR-2003.
 PD
 XX
 XX 22-AUG-2002; 2002WO-US027145.
 PF
 XX
 XX 28-AUG-2001; 2001US-00942024.
 PR
 XX
 XX (ALLR) ALLERGAN INC.
 PA
 XX Steward LE, Fernandez-Salas E, Aoki KR;
 PI
 XX WPI; 2003-290198/28.
 DR
 XX
 XX Botulinum serotype A/E substrate useful for assaying protease activity of
 PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 PT toxin recognition sequence that includes a cleavage site.
 PT
 XX
 XX Disclosure; Page 42; 168pp; English.

CC The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is goldfish
 CC SNAP-25B peptide used in the invention
 XX
 XX Sequence 33 AA;

Query Match 100.0%; Score 84; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
 |||||
 Db 17 TRIDEANQRATKMLGSG 33

RESULT 15
 AAE36678
 ID AAE36678 standard; peptide; 33 AA.
 XX
 AC AAE36678;

XX 07-AUG-2003 (first entry)
 DT
 XX SNAP-25 peptide.
 DE

XX Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW cosmetic; mouse; rat.
 XX

OS Homo sapiens.
 OS Mus musculus.
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 7. .8
 FT /note= "BoNT/E sensitive cleavage site"
 FT Cleavage-site 24. .25
 FT /note= "BoNT/A sensitive cleavage site"
 FT Cleavage-site 25. .26
 FT /note= "BoNT/C sensitive cleavage site"
 FT

XX WO2003020948-A2.

PN

XX 13-MAR-2003.

XX 22-AUG-2002; 2002WO-US027145.

XX 28-AUG-2001; 2001US-00942024.

XX (ALLR) ALLERGAN INC.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-290198/28.

XX Botulinum serotype A/E substrate useful for assaying protease activity of

PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial

PT toxin recognition sequence that includes a cleavage site.

PT Disclosure; Page 42; 168pp; English.

XX The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is SNAP-25
 CC peptide used in the invention
 XX
 XX Sequence 33 AA;

Query Match 100.0%; Score 84; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRIDEANQRATKMLGSG 18
 |||||
 Db 17 TRIDEANQRATKMLGSG 33

Search completed: April 3, 2006, 15:36:57
 Job time : 97.607 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM protein - protein search, using sw model

Run on: April 3, 2006, 15:30:10 ; Search time 11.9083 Seconds

(without alignments)
177.756 Million cell updates/sec

Title: US-09-942-098-93

Perfect score: 99

Sequence: 1 XMEKTRIDEANQRATKMLGSGX 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	89.9	203	2 I50481	synapse protein SN
2	89	89.9	204	2 I50480	synapse protein SN
3	89	89.9	206	2 A37861	synaptosomal-assoc
4	89	89.9	206	2 I53735	nerve terminal pro
5	89	89.9	206	2 I67823	nerve terminal pro
6	89	89.9	206	2 A33623	synaptosomal-assoc
7	64	64.6	210	2 I50552	synapse protein -
8	51	51.5	29	2 A49708	synaptosomal-assoc
9	49	49.5	296	2 D87525	conserved hypothe
10	47.5	48.0	1361	2 A29959	DNA-directed RNA p
11	46	46.5	210	2 JC5512	SNARE protein 23 -
12	46	46.5	1578	2 S76238	hypothetical prote
13	46	46.5	2288	2 T29999	hypothetical prote
14	45	45.5	393	2 T32127	hypothetical prote
15	45	45.5	642	2 G30551	lipoprotein (impor
16	44	44.4	278	2 AH3356	cone oporon protei
17	44	44.4	745	2 D96829	homeobox protein (
18	44	44.4	747	2 S71478	homeotic protein A
19	44	44.4	829	2 I40014	sorbitol dehydroge
20	42.5	42.9	1056	2 T33167	hypothetical prote
21	42	42.4	83	2 A33854	outer membrane lip
22	42	42.4	125	2 G29826	hypothetical 13.9K
23	42	42.4	139	2 AE1918	hypothetical prote
24	42	42.4	158	2 JC5297	vesicle-membrane f
25	42	42.4	211	2 JC5296	vesicle-membrane f
26	42	42.4	536	2 AI0063	probable OmpA-fam
27	42	42.4	575	2 F69666	methyl-accepting c
28	42	42.4	1692	2 A33988	adenylate cyclase
29	41.5	41.9	377	2 A53279	serotonin receptor

30 41 41.4 221 2 T10751
31 41 41.4 323 2 T12892
32 41 41.4 494 2 S64386
33 41 41.4 503 2 T35053
34 41 41.4 542 2 T23869
35 41 41.4 563 2 T21529
36 41 41.4 602 2 T23386
37 41 41.4 609 2 T52524
38 41 41.4 639 2 T16648
39 41 41.4 679 2 E71282
40 41 41.4 704 2 S25586
41 41 41.4 740 2 G75477
42 41 41.4 930 2 T34334
43 40.5 40.9 431 2 T45246
44 40.5 40.9 449 2 C87066
45 40.5 40.9 540 2 T34187

MADS-box protein M
ATP/GTP binding pr
pre-mRNA splicing
probable solute-bi
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
probable general s
lcrD protein - Yer
probable general s
hypothetical prote
probable histidino
histidinol dehydro
hypothetical prote

ALIGNMENTS

RESULT 1

I50481

synapse protein SNAP-25 - goldfish

C;Species: Carassius auratus (goldfish)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C;Accession: I50481

R;Risinger, C.; Larhammar, D.

Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993

A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.

A;Reference number: A49632; MUID:94068448; PMID:8248151

A;Accession: I50481

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-203 <RIS>

A;Cross-references: UNIPROT:P36978; UNIPARC:UPI0000135B03; GB:L22976; NID:G349430; PIDN:?

C;Genetics:

A;Gene: SNAP-25

Query Match 89.9%; Score 89; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KTRIDEANQRATKMLGSG 21

|||||

Db 186 KTRIDEANQRATKMLGSG 203

RESULT 2

I50480

synapse protein SNAP-25 - goldfish

C;Species: Carassius auratus (goldfish)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C;Accession: I50480

R;Risinger, C.; Larhammar, D.

Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993

A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.

A;Reference number: A49632; MUID:94068448; PMID:8248151

A;Accession: I50480

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-204 <RIS>

A;Cross-references: UNIPROT:P36977; UNIPARC:UPI0000135B02; GB:L22973; NID:G349426; PIDN:?

C;Genetics:

A;Gene: SNAP-25

Query Match 89.9%; Score 89; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KTRIDEANQRATKMLGSG 21

|||||

Db 187 KTRIDEANQRATKMLGSG 204

RESULT 3

A37861
synaptosomal-associated 25K protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
C;Accession: A37861
R;Catsicas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coincides with the expression of synaptophysin in the developing rat brain.
A;Reference number: A37861; MUID:91126080; PMID:1992470
A;Accession: A37861
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <CAT>
A;Cross-references: UNIPROT:P60878; UNIPARC:UPI0000001103; GB:M57957; NID:g212673; PIDN:f

Query Match 89.9%; Score 89; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
|||||
Db 189 KTRIDEANQRATKMLGSG 206

RESULT 4

I53735
nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I53735
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein.
A;Reference number: I53735; MUID:94156217; PMID:8112622
A;Accession: I53735
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: UNIPROT:P60880; UNIPARC:UPI000002B3DD; GB:L19760; NID:g307425; PIDN:f

C;Genetics:
A;Gene: GDB:SNAP
A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2

Query Match 89.9%; Score 89; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
|||||
Db 189 KTRIDEANQRATKMLGSG 206

RESULT 5

I67823
nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I67823
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994

A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein.
A;Reference number: I53735; MUID:94156217; PMID:8112622
A;Accession: I67823
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: UNIPROT:P60880; UNIPARC:UPI0000001103; GB:L19761; NID:g307427; PIDN:f
C;Genetics:
A;Gene: GDB:SNAP

A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2

Query Match 89.9%; Score 89; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
|||||
Db 189 KTRIDEANQRATKMLGSG 206

RESULT 6

A33623
synaptosomal-associated 25K protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 09-Jul-2004
C;Accession: A33623
R;Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.; J.
Cell Biol. 109, 3039-3052, 1989

A;Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differs from the previously identified synaptophysin.
A;Reference number: A33623; MUID:90078337; PMID:2592413
A;Accession: A33623
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <OYL>
A;Cross-references: UNIPROT:P60879; UNIPARC:UPI0000001103; GB:M22012; GB:X51673; NID:g201

Query Match 89.9%; Score 89; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
|||||
Db 189 KTRIDEANQRATKMLGSG 206

RESULT 7

I50552
synapse protein - marbled electric ray
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50552
R;Risager, C.; Blomqvist, A.G.; Lundell, I.; Lambertsson, A.; Nassel, D.; Pieribone, V.F.
J. Biol. Chem. 268, 24408-24414, 1993
A;Title: Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25) shk
A;Reference number: A49513; MUID:94043281; PMID:8226991
A;Accession: I50552
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-210 <RIS>
A;Cross-references: UNIPROT:P36976; UNIPARC:UPI0000135AFE; GB:L22020; NID:g431296; PIDN:f

Query Match 64.6%; Score 64; DB 2; Length 210;
Best Local Similarity 76.5%; Pred. No. 0.0043;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 MEKTRIDEANQRATKML 18
|||||
Db 194 MNKARIDEANKHATKML 210

RESULT 8

A49708
synaptosomal-associated 25K protein - rat (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 12-Jun-1998
C;Accession: A49708
R;Binz, T.; Blas, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.; J.
Biol. Chem. 269, 1617-1620, 1994
A;Title: Proteolysis of SNAP-25 by types E and A botulinum neurotoxins.
A;Reference number: A49708; MUID:94124495; PMID:8294407
A;Accession: A49708

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-29 <BIN>
A;Cross-references: UNIPARC:UPI000017C9D4

Query Match 51.5%; Score 51; DB 2; Length 29;
Best Local Similarity 65.0%; Pred. No. 0.074;
Matches 13; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

QY 2 MEKTRIDEANQRATKMLGSG 21
||| | |||||
DB 12 MEKA--DSNKRTRATKMLGSG 29
||| | |||||

RESULT 9
D87525 conserved hypothetical protein CC2229 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D87525
R;Niernan, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87525
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-296 <STO>
A;Cross-references: UNIPROT:Q9A665; UNIPARC:UPI00000C765E; GB:AE005673; NID:gl3423736; F
C;Genetics:
A;Gene: CC2229

Query Match 49.5%; Score 49; DB 2; Length 296;
Best Local Similarity 55.6%; Pred. No. 2;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
| : ||| || : |||
DB 247 KRNVDWANQLTKLAGSG 264
| : ||| || : |||

RESULT 10
A29959 DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - spinach chloroplast
C;Species: chloroplast Spinacia oleracea (spinach)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29959
R;Hudson, G.S.; Holton, T.A.; Whitfield, P.R.; Bottomley, W.
J. Mol. Biol. 200, 639-654, 1988
A;Title: Spinach chloroplast rpoBC genes encode three subunits of the chloroplast RNA po
A;Reference number: A29959; MUID:88316931; PMID:3045324
A;Accession: A29959
A;Molecule type: DNA
A;Residues: 1-1361 <HUD>
A;Cross-references: UNIPROT:P11704; UNIPARC:UPI0000134774; EMBL:M55297; NID:g295119; PID
C;Genetics:
A;Gene: rpoC-2
A;Genome: chloroplast
C;Superfamily: chloroplast DNA-directed RNA polymerase beta'-2 chain
C;Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 48.0%; Score 47.5; DB 2; Length 1361;
Best Local Similarity 57.9%; Pred. No. 19;
Matches 11; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 2 MEKTRIDEANQRATKMLGS 20
: ||| ||| : ||| |||
DB 1153 LEK-RIDSWNERITRLGS 1170
: ||| ||| : ||| |||

RESULT 11

JC5512 SNARE protein 23 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5512
R;Araki, S.; Tamori, Y.; Kawanishi, M.; Shinoda, H.; Masugi, J.; Mori, H.; Niki, T.; Oka;
Biochem. Biophys. Res. Commun. 234, 257-262, 1997
A;Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c.
A;Reference number: JC5512; MUID:97312558; PMID:9168999
A;Accession: JC5512
A;Molecule type: mRNA
A;Residues: 1-210 <ARA>
A;Cross-references: UNIPROT:O09044; UNIPARC:UPI0000022B5C; DBJ:AB000822; NID:g2189950; f
C;Comment: This protein is involved in the insulin-induced translocation of vesicles cont

Query Match 46.5%; Score 46; DB 2; Length 210;
Best Local Similarity 58.8%; Pred. No. 4.4;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGS 20
||| | ||||| : :
DB 194 KNRIDIANTRAKKLIDS 210
||| | ||||| : : |

RESULT 12
S76238 hypothetical protein sll0267 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
S.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76238
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1578 <KAN>
A;Cross-references: UNIPROT:P74400; UNIPARC:UPI00000C10E9; EMBL:D90914; GB:AB001339; NID:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 46.5%; Score 46; DB 2; Length 1578;
Best Local Similarity 44.4%; Pred. No. 39;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 MEKTRIDEANQRATKMLG 19
: : ||| |||
DB 1000 LDAIQLDQANQANQLG 1017
: : ||| |||

RESULT 13
T29999 hypothetical protein ZC8.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29999
R;Latreille, P.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid ZC8.
A;Reference number: Z20719
A;Accession: T29999
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2288 <LAT>
A;Cross-references: UNIPROT:Q23081; UNIPARC:UPI000017BCE7; EMBL:U64862; PIDN:AAB52624.1;
A;Experimental source: strain Bristol N2; clone ZC8
C;Genetics:
A;Gene: CESP:ZC8.4
A;Map position: X
A;Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 1686/1

Query Match 46.5%; Score 46; DB 2; Length 2288;
Best Local Similarity 60.0%; Pred. No. 59;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 KTRIDEANORATKML 18
|||||:|:
DB 626 KTRIDELNRRVENLL 640

RESULT 14

T32127
hypothetical protein R07C3.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32127
R;Lamar, B.; Kramer, J.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid R07C3.
A;Reference number: Z21125
A;Accession: T32127
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393 <LAM>
A;Cross-references: UNIPROT:O16766; UNIPARC:UPI00001642E9; EMBL:AF016686; PIDN:AAB66239.
A;Experimental source: strain Bristol N2; clone R07C3
C;Genetics:
A;Gene: CESP:R07C3.10
A;Map position: 2
A;Introns: 20/1; 350/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C32B5.10

Query Match 45.5%; Score 45; DB 2; Length 393;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EKTRIDEANORATKM 17
|||:|:
DB 98 EKWKIKENEKITKM 112

RESULT 15

G90551
lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: G90551
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissou, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: G90551
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-642 <KUR>
A;Cross-references: UNIPROT:Q98QP2; UNIPARC:UPI00000C8060; GB:AL445566; PID:gl4089733; E
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU 3190
A;Genetic code: SGC3

Query Match 45.5%; Score 45; DB 2; Length 642;
Best Local Similarity 44.4%; Pred. No. 22;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 KTRIDEANORATKMLGSG 21
|||:|:
DB 216 KTKIDQANQKNTSIPEG 233

Search completed: April 3, 2006, 15:31:20
Job time : 12.9083 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:27:08 ; Search time 112.826 Seconds
(without alignments)
85.675 Million cell updates/sec

Title: US-09-942-098-93

Perfect score: 99

Sequence: 1 XMEKTRIDEANQRATNMGSGX 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A Geneseq 21:*
- 1: geneseqp1980s:*
 - 2: geneseqp1990s:*
 - 3: geneseqp2000s:*
 - 4: geneseqp2001s:*
 - 5: geneseqp2002s:*
 - 6: geneseqp2003as:*
 - 7: geneseqp2003bs:*
 - 8: geneseqp2004s:*
 - 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	100.0	22	6 AAE36738	Aae36738 Fret subs
2	99	100.0	22	7 ABW01794	Abw01794 FRET subs
3	89	89.9	19	6 AAE36740	Aae36740 Fret subs
4	89	89.9	19	6 AAE36737	Aae36737 Fret subs
5	89	89.9	19	7 ABW01793	Abw01793 FRET subs
6	89	89.9	19	7 ABW01796	Abw01796 FRET subs
7	89	89.9	20	2 AAW30100	Aaw30100 Neurotran
8	89	89.9	23	6 AAE36733	Aae36733 Fret subs
9	89	89.9	23	7 ABW01789	Abw01789 FRET subs
10	89	89.9	24	6 AAE36735	Aae36735 Fret subs
11	89	89.9	24	7 ABW01791	Abw01791 FRET subs
12	89	89.9	26	2 AAW30099	Aaw30099 Neurotran
13	89	89.9	33	6 AAE36682	Aae36682 Goldfish
14	89	89.9	33	6 AAE36683	Aae36683 Goldfish
15	89	89.9	33	6 AAE36678	Aae36678 SNAP-25 p
16	89	89.9	33	7 ABW01739	Abw01739 Goldfish
17	89	89.9	33	7 ABW01734	Abw01734 Mouse SNA
18	89	89.9	33	7 ABW01738	Abw01738 Goldfish
19	89	89.9	33	8 ADM97054	Adm97054 Botulinum
20	89	89.9	33	8 ADM97053	Adm97053 Botulinum
21	89	89.9	33	8 ADM97049	Adm97049 Botulinum
22	89	89.9	33	9 AEA14927	Aea14927 Goldfish
23	89	89.9	33	9 AEA14923	Aea14923 SNAP-25 s
24	89	89.9	33	9 AEA14928	Aea14928 Goldfish

ALIGNMENTS

RESULT 1

AAE36738
ID AAE36738 standard; peptide; 22 AA.

XX AC AAE36738;

XX 07-AUG-2003 (first entry)

XX Fret substrate peptide #9 used in the invention.

XX Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
XX tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
XX cosmetic.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1

FT /note= "Fluorescein-modified Lysine; This residue is
FT given as Xaa in the sequence shown as SEQ ID NO: 93 in
FT the sequence listing of the specification"

FT Modified-site 22

FT /note= "Tetramethylrhodamine-modified Lysine; C-terminal
FT amide; This residue is given as Xaa in the sequence shown
FT as SEQ ID NO: 93 in the sequence listing of the
FT specification"

WO2003020948-A2.

13-MAR-2003.

22-AUG-2002; 2002WO-US027145.

28-AUG-2001; 2001US-00942024.

(ALLR) ALLERGAN INC.

Steward LE, Fernandez-Salas E, Aoki KR;

WPI; 2003-290198/28.

Botulinum serotype A/E substrate useful for assaying protease activity of
botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
toxin recognition sequence that includes a cleavage site.

Example 1; Page 115; 168pp; English.

CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is fret
 CC substrate peptide used in the exemplification of the invention
 XX
 SQ

Query Match 89.9%; Score 89; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
 |||||
 Db 1 KTRIDEANQRATKMLGSG 18

RESULT 4
 AAE36737
 ID AAE36737 standard; peptide; 19 AA.

XX AAE36737;

XX 07-AUG-2003 (first entry)

XX Fret substrate peptide #8 used in the invention.

XX Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW cosmetic.

XX Unidentified.

XX Key Location/Qualifiers
 FT Modified-site 1

FT /note= "Fluorescein-modified lysine; This residue is
 FT given as Xaa in the sequence shown as SEQ ID NO: 92 in
 FT the sequence listing of the specification"

FT Modified-site 19
 FT /note= "Tetramethylrhodamine-modified lysine; C-terminal
 FT amide; This residue is given as Xaa in the sequence shown
 FT as SEQ ID NO: 92 in the sequence listing of the
 FT specification"

XX WO2003020948-A2.

XX 13-MAR-2003.

XX 22-AUG-2002; 2002WO-US027145.

XX 28-AUG-2001; 2001US-00942024.

XX (ALLR) ALLERGAN INC.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-290198/28.

XX Botulinum serotype A/E substrate useful for assaying protease activity of
 PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 PT toxin recognition sequence that includes a cleavage site.

PS Example 1; Page 115; 16pp; English.

XX

CC The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is fret
 CC substrate peptide used in the exemplification of the invention
 XX
 SQ

Query Match 89.9%; Score 89; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
 |||||
 Db 1 KTRIDEANQRATKMLGSG 18

RESULT 5

ABW01793
 ID ABW01793 standard; peptide; 19 AA.

XX ABW01793;

XX 12-FEB-2004 (first entry)

XX FRET substrate #6 to analyse proteolytic activity of botulinum toxin.

XX Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
 KW FRET; fluorescence resonance energy transfer.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Fluorescein-labeled lysine"

FT Modified-site 19 /note= "Tetramethylrhodamine labelled lysine; C-terminal
 FT amide"

FT US2003143651-A1.

XX 31-JUL-2003.

XX 28-AUG-2001; 2001US-00942098.

XX 28-AUG-2001; 2001US-00942098.

XX (STEW/) STEWARD L E.

XX (FERN/) FERNANDEZ-SALAS E.

XX (AOKI/) AOKI K R.

XX Steward LE, Fernandez-Salas E, Aoki KR;

XX WPI; 2003-829791/77.

XX Determining clostridial toxin protease activity, by treating sample with
 PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
 PT sequence, under conditions which exhibit resonance energy transfer.

```

XX Example 1; Page 29; Opp; English.
PS
CC The present invention provides clostridial toxin substrates useful in
CC assaying for the protease activity of any clostridial toxin including
CC toxins of all serotypes as well as tetanus toxins. The present sequence
CC is FRET (fluorescence resonance energy transfer) substrate to analyse
CC proteolytic activity of botulinum toxin. This substrate is used in the
CC exemplification of the invention
XX
XX Sequence 19 AA;
  Query Match      89.9%; Score 89; DB 7; Length 19;
  Best Local Similarity 100.0%; Pred. No. 1.5e-07;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 4 KTRIDEANQRATKMLGSG 21
  Db 1 KTRIDEANQRATKMLGSG 18
      |||||
RESULT 6
ABW01796
ID AEW01796 standard; peptide; 19 AA.
AC AEW01796;
XX
XX 12-FEB-2004 (first entry)
DT
DE
DE FRET substrate #9 to analyse proteolytic activity of botulinum toxin.
XX
XX Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
KW FRET; fluorescence resonance energy transfer.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT Modified-site 19
FT Modified-site 19 /note= "DABCYL labelled lysine"
FT Modified-site 19 /note= "EDANS labelled lysine; C-terminal amide"
XX
XX US2003143651-A1.
XX
XX 31-JUL-2003.
PD
XX
XX 28-AUG-2001; 2001US-00942098.
XX
XX 28-AUG-2001; 2001US-00942098.
XX
XX (STEW/) STEWARD L E.
PA (FERN/) FERNANDEZ-SALAS E.
PA (AOKI/) AOKI K R.
XX
XX Steward LE, Fernandez-Salas E, Aoki KR;
PI
DR WPI; 2003-829791/77.
XX
XX Determining clostridial toxin protease activity, by treating sample with
PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
PT sequence, under conditions which exhibit resonance energy transfer.
XX
XX Example 1; Page 29; Opp; English.
PS
XX The present invention provides clostridial toxin substrates useful in
CC assaying for the protease activity of any clostridial toxin including
CC toxins of all serotypes as well as tetanus toxins. The present sequence
CC is FRET (fluorescence resonance energy transfer) substrate to analyse
CC proteolytic activity of botulinum toxin. This substrate is used in the
CC exemplification of the invention
XX
XX Sequence 19 AA;
  Query Match      89.9%; Score 89; DB 7; Length 19;
  Best Local Similarity 100.0%; Pred. No. 1.5e-07;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 4 KTRIDEANQRATKMLGSG 21
  Db 1 KTRIDEANQRATKMLGSG 18
      |||||

```

```

  Query Match      89.9%; Score 89; DB 7; Length 19;
  Best Local Similarity 100.0%; Pred. No. 1.5e-07;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 4 KTRIDEANQRATKMLGSG 21
  Db 1 KTRIDEANQRATKMLGSG 18
      |||||
RESULT 7
AAW30100
ID AAW30100 standard; peptide; 20 AA.
XX
XX AAW30100;
AC
XX 06-APR-1998 (first entry)
DT
DE
DE Neurotransmitter secretion inhibitor #4.
XX
XX Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
KW excitation-secretory uncoupling peptide; catecholamine secretion;
KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
KW synaptosomal associated protein; SNAP-25.
XX
XX Homo sapiens.
XX
XX WO9734620-A1.
PN
XX
XX 25-SEP-1997.
PD
XX
XX 18-MAR-1997; 97WO-US0004393.
PF
XX
XX 18-MAR-1996; 96US-0013599P.
PR
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX
XX Montal M;
PI
XX
XX WPI; 1997-479986/44.
DR
XX
XX Excitation-secretory uncoupling peptide(s) for inhibiting
PT neuro:transmitter release - used particularly for treating muscle
PT spasticity, and for delivering drugs specifically to neural cells.
XX
XX Claim 14; Page 32; 61pp; English.
PS
XX
XX This sequence corresponds to residues 187-206 of the human 25 kD
CC synaptosomal associated protein (SNAP-25), and is an inhibitory agent of
CC the invention. The agents of the invention inhibit secretion of
CC neurotransmitter from neuronal cells and is an excitation-secretory
CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which
CC correspond substantially to any one of AAW30097-W30102, or more generally
CC any (I) that inhibits 50% of catecholamine secretion from bovine
CC chromaffin cells at a concentration of 10 microm, especially 0.25 microm,
CC or less. (I) are used, as a replacement for Clostridium toxin, to inhibit
CC release of neurotransmitters from synaptic vesicles, specifically for
CC reducing muscle spasticity. Also (I) may be labelled to allow in vivo
CC imaging of intracellular distribution of (I). Compounds for delivering
CC the drug to neural cells provide targeted drug delivery, e.g. of
CC substance P to brain tumours for induction of apoptosis. Unlike the
CC neurotoxins, (I) are not toxic or immunogenic and are more readily
CC available. Their therapeutic effect lasts for several days or weeks, so
CC lower doses or less frequent treatments are required
XX
XX Sequence 20 AA;
  Query Match      89.9%; Score 89; DB 2; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.6e-07;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 4 KTRIDEANQRATKMLGSG 21
  Db 3 KTRIDEANQRATKMLGSG 20
      |||||

```

```
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

4 KTRIDEANQRATKMLGSG 21
|||||
5 KTRIDEANQRATKMLGSG 22

RESULT 9
ABW01789
ABW01789 standard; peptide; 23 AA.
ABW01789;
12-FEB-2004 (first entry)
FRET substrate #2 to analyse proteolytic activity of botulinum toxin.
Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
FRET; fluorescence resonance energy transfer.
Unidentified.
Key Location/Qualifiers
Modified-site 1 /note= "Fluoresceinated lysine"
Modified-site 23 /note= "Tetramethylrhodamine labelled lysine; C-terminal amide"
US2003143651-A1.
31-JUL-2003.
28-AUG-2001; 2001US-00942098.
28-AUG-2001; 2001US-00942098.
(STEW/) STEWARD L E.
(FERN/) FERNANDEZ-SALAS E.
(AOKI/) AOKI K R.
Steward LE, Fernandez-Salas E, Aoki KR;
WPI; 2003-829791/77.
Determining clostridial toxin protease activity, by treating sample with clostridial substrate with donor fluorophore, acceptor, toxin recognition sequence, under conditions which exhibit resonance energy transfer.
Example 1; Page 29; Opp; English.
The present invention provides clostridial toxin substrates useful in assaying for the protease activity of any clostridial toxin including toxins of all serotypes as well as tetanus toxins. The present sequence is FRET (fluorescence resonance energy transfer) substrate to analyse proteolytic activity of botulinum toxin. This substrate is used in the exemplification of the invention
Sequence 23 AA;
Query Match 89.9%; Score 89; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
4-KTRIDEANQRATKMLGSG 21
|||||
5 KTRIDEANQRATKMLGSG 22

RESULT 10

```

AE36735 standard; peptide; 24 AA.

AE36735 standard; peptide; 24 AA.

XX AAE36735;
XX 07-AUG-2003 (first entry)
XX Fret substrate peptide #6 used in the invention.
XX Clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
XX tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
XX cosmetic.
XX Unidentified.
XX OS Location/Qualifiers
XX FH
XX Key
XX Modified-site 1 /note= "Fluorescein-modified Lysine; This residue is
FT given as Xaa in the sequence shown as SEQ ID NO: 90 in
FT the sequence listing of the specification"
FT Modified-site 24
FT /note= "Tetramethylrhodamine-modified Lysine; C-terminal
FT amide; This residue is given as Xaa in the sequence shown
FT as SEQ ID NO: 90 in the sequence listing of the
FT specification"
XX WO2003020948-A2.
XX 13-MAR-2003.
XX 22-AUG-2002; 2002WO-US027145.
XX 28-AUG-2001; 2001US-00942024.
XX (ALLR) ALLERGAN INC.
XX Steward LE, Fernandez-Salas E, Aoki KR;
XX WPI; 2003-290198/28.
XX Botulinum serotype A/E substrate useful for assaying protease activity of
PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
PT toxin recognition sequence that includes a cleavage site.
XX Example 1; Page 115; 168pp; English.
XX The present invention relates to novel clostridium toxin substrates. The
CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
CC which comprise a donor fluorophore, an acceptor having an absorbance
CC spectrum overlapping the emission spectrum of the donor fluorophore and a
CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
CC the cleavage site intervenes between the donor fluorophore and acceptor
CC and under the appropriate conditions, the resonance energy transfer is
CC exhibited between the donor and acceptor. Natural targets of clostridium
CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
CC of the invention are useful in assaying for the protease activity of any
CC clostridial toxin including botulinum toxins of all serotypes and tetanus
CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
CC samples, water samples, cosmetics, tissue samples and beverage or food
CC samples. They are useful to assay a sample from a human or animal, for
CC e.g., exposed to clostridial toxin or having one or more symptoms of a
CC clostridial toxin, to follow activity during production and purification
CC of clostridial toxin and to assay formulated clostridial toxin products
CC including pharmaceuticals and cosmetics. The present sequence is fret
CC substrate peptide used in the exemplification of the invention
XX SQ Sequence 24 AA;
XX Query Match 89.9%; Score 89; DB 6; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 KTRIDEANQRATKMLGSG 21
|||||

Db 6 KTRIDEANQRATKMLGSG 23
RESULT 11
ABW01791
ID ABW01791 standard; peptide; 24 AA.
XX ABW01791,
XX 12-FEB-2004 (first entry)
XX FRET substrate #4 to analyse proteolytic activity of botulinum toxin.
XX Clostridial toxin; protease activity; tetanus toxin; botulinum toxin;
KW FRET; fluorescence resonance energy transfer.
XX Unidentified.
XX Key Location/Qualifiers
XX Modified-site 1 /note= "Fluoresceinated lysine"
FT Modified-site 24
FT /note= "Tetramethylrhodamine labelled lysine; C-terminal
FT amide"
XX US2003143651-A1.
XX 31-JUL-2003.
XX 28-AUG-2001; 2001US-00942098.
XX 28-AUG-2001; 2001US-00942098.
XX (STEW/) STEWARD L E.
XX (FERN/) FERNANDEZ-SALAS E.
XX (AOKI/) AOKI K R.
XX Steward LE, Fernandez-Salas E, Aoki KR;
XX WPI; 2003-829791/77.
XX Determining clostridial toxin protease activity, by treating sample with
PT clostridial substrate with donor fluorophore, acceptor, toxin recognition
PT sequence, under conditions which exhibit resonance energy transfer.
XX Example 1; Page 29; Opp; English.
XX The present invention provides clostridial toxin substrates useful in
CC assaying for the protease activity of any clostridial toxin including
CC toxins of all serotypes as well as tetanus toxins. The present sequence
CC is FRET (fluorescence resonance energy transfer) substrate to analyse
CC proteolytic activity of botulinum toxin. This substrate is used in the
CC exemplification of the invention
XX SQ Sequence 24 AA;
XX Query Match 89.9%; Score 89; DB 7; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 KTRIDEANQRATKMLGSG 21
|||||
Db 6 KTRIDEANQRATKMLGSG 23
RESULT 12
AAW30099
ID AAW30099 standard; peptide; 26 AA.
XX AAW30099;
XX 06-APR-1998 (first entry)
XX

DE Neurotransmitter secretion inhibitor #3.
XX Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
KW excitation-secretory uncoupling peptide; catecholamine secretion;
KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
KW synaptosomal associated protein; SNAP-25.
XX Homo sapiens.
XX WO9734620-A1.
XX 25-SEP-1997.
XX 18-MAR-1997; 97WO-US004393.
XX 18-MAR-1996; 96US-0013599P.
XX (REGC) UNIV CALIFORNIA.
XX Montal M;
XX WPI; 1997-479986/44.
XX Excitation-secretory uncoupling peptide(s) for inhibiting
PT neurotransmitter release - used particularly for treating muscle
PT spasticity, and for delivering drugs specifically to neural cells.
XX Claim 13; Page 31; 61pp; English.
XX This sequence corresponds to residues 181-206 of the human 25 kD
CC synaptosomal associated protein (SNAP-25), and is an inhibitory agent of
CC the invention. The agents of the invention inhibit secretion of
CC neurotransmitter from neuronal cells and is an excitation-secretory
CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which
CC correspond substantially to any one of AAM30097-W30102, or more generally
CC any (I) that inhibits 50% of catecholamine secretion from bovine
CC chromaffin cells at a concentration of 10 microm, especially 0.25 microm,
CC or less. (I) are used, as a replacement for Clostridium toxin, to inhibit
CC release of neurotransmitters from synaptic vesicles, specifically for
CC reducing muscle spasticity. Also (I) may be labelled to allow in vivo
CC imaging of intracellular distribution of (I). Compounds for delivering
CC the drug to neural cells provide targeted drug delivery, e.g. of
CC substance P to brain tumours for induction of apoptosis. Unlike the
CC neurotoxins, (I) are not toxic or immunogenic and are more readily
CC available. Their therapeutic effect lasts for several days or weeks, so
CC lower doses or less frequent treatments are required
XX Sequence 26 AA;
SQ

Query Match 89.9%; Score 89; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.1e-07; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 4 KTRIDEANQRATKMLGSG 21
Db 9 KTRIDEANQRATKMLGSG 26

RESULT 13
AAE36682
ID AAE36682 standard; peptide; 33 AA.

XX AAE36682;
XX 07-AUG-2003 (first entry)
XX Goldfish SNAP-25A peptide.

XX Goldfish; clostridium toxin; protease activity; botulinum toxin; BONT;
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
KW TeNT; cosmetic.
XX Carassius auratus.

XX Key Location/Qualifiers
FH Cleavage-site 7..8
FT /note= "BONT/E sensitive cleavage site"
FT Cleavage-site 24..25
FT /note= "BONT/A sensitive cleavage site"
FT Cleavage-site 25..26
FT /note= "BONT/C sensitive cleavage site"
XX WO2003020948-A2.
XX 13-MAR-2003.
XX 22-AUG-2002; 2002WO-US027145.
XX 28-AUG-2001; 2001US-00942024.
XX (ALLR) ALLERGAN INC.
XX Steward LE, Fernandez-Salas E, Aoki KR;
XX WPI; 2003-290198/28.
XX Botulinum serotype A/E substrate useful for assaying protease activity of
PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
PT toxin recognition sequence that includes a cleavage site.
XX Disclosure; Page 42; 168pp; English.

XX The present invention relates to novel clostridium toxin substrates. The
CC invention further relates to botulinum serotype A/E (BONT/A/E) substrates
CC which comprise a donor fluorophore, an acceptor having an absorbance
CC spectrum overlapping the emission spectrum of the donor fluorophore and a
CC BONT A or BONT/E recognition sequence comprising a cleavage site, where
CC the cleavage site intervenes between the donor fluorophore and acceptor
CC and under the appropriate conditions, the resonance energy transfer is
CC exhibited between the donor and acceptor. Natural targets of clostridium
CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
CC of the invention are useful in assaying for the protease activity of any
CC clostridial toxin including botulinum toxins of all serotypes and tetanus
CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
CC samples, water samples, cosmetics, tissue samples and beverage or food
CC samples. They are useful to assay a sample from a human or animal, for
CC e.g., exposed to clostridial toxin or having one or more symptoms of a
CC clostridial toxin, to follow activity during production and purification
CC of clostridial toxin and to assay formulated clostridial toxin products
CC including pharmaceuticals and cosmetics. The present sequence is goldfish
CC SNAP-25A peptide used in the invention

XX Sequence 33 AA;

Query Match 89.9%; Score 89; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.7e-07; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 4 KTRIDEANQRATKMLGSG 21
Db 16 KTRIDEANQRATKMLGSG 33

RESULT 14
AAE36683
ID AAE36683 standard; peptide; 33 AA.

XX AAE36683;
XX 07-AUG-2003 (first entry)
XX Goldfish SNAP-25B peptide.

XX Goldfish; clostridium toxin; protease activity; botulinum toxin; BONT;
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
KW SNAP-25A peptide used in the invention

```

KW TeNT; cosmetic.
XX
OS Carassius auratus.
XX
FH Key Location/Qualifiers
FT Cleavage-site 7..8
FT /note= "BoNT/E sensitive cleavage site"
FT Cleavage-site 24..25
FT /note= "BoNT/A sensitive cleavage site"
FT Cleavage-site 25..26
FT /note= "BoNT/C sensitive cleavage site"
XX
XX WO2003020948-A2.
XX
XX 13-MAR-2003.
XX
XX 22-AUG-2002; 2002WO-US027145.
XX
XX 28-AUG-2001; 2001US-00942024.
XX
XX (ALLR ) ALLERGAN INC.
XX
XX Steward LE, Fernandez-Salas E, Aoki KR;
XX
XX WPI; 2003-290198/28.
XX
XX Botulinum serotype A/E substrate useful for assaying protease activity of
XX botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
XX toxin recognition sequence that includes a cleavage site.
XX
XX Disclosure; Page 42; 168pp; English.
XX
XX The present invention relates to novel clostridium toxin substrates. The
XX invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
XX which comprise a donor fluorophore, an acceptor having an absorbance
XX spectrum overlapping the emission spectrum of the donor fluorophore and a
XX BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
XX the cleavage site intervenes between the donor fluorophore and acceptor
XX and under the appropriate conditions, the resonance energy transfer is
XX exhibited between the donor and acceptor. Natural targets of clostridium
XX neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
XX of the invention are useful in assaying for the protease activity of any
XX clostridial toxin including botulinum toxins of all serotypes and tetanus
XX toxins (TeNT) in a sample including bacterial, baculoviral and yeast
XX lysate, raw, cooked or processed foods, beverages, animal feed, soil
XX samples, water samples, cosmetics, tissue samples and beverage or food
XX samples. They are useful to assay a sample from a human or animal, for
XX e.g., exposed to clostridial toxin or having one or more symptoms of a
XX clostridial toxin, to follow activity during production and purification
XX of clostridial toxin and to assay formulated clostridial toxin products
XX including pharmaceuticals and cosmetics. The present sequence is goldfish
XX SNAP-25B peptide used in the invention
XX
XX Sequence 33 AA;
XX
XX Query Match 89.9%; Score 89; DB 6; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4 KTRIDEANQRATKMLGSG 21
XX |||||||
XX 16 KTRIDEANQRATKMLGSG 33
XX
XX RESULT 15
XX AAE36678
XX ID AAE36678 standard; peptide; 33 AA.
XX
XX AC AAE36678;
XX
XX 07-AUG-2003 (first entry)
XX
XX DE SNAP-25 peptide.
XX
XX Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
XX tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
XX cosmetic; mouse; rat.
XX
XX Homo sapiens.
XX Mus musculus.
XX Rattus sp.
XX
XX Key Location/Qualifiers
XX Cleavage-site 7..8
XX /note= "BoNT/E sensitive cleavage site"
XX Cleavage-site 24..25
XX /note= "BoNT/A sensitive cleavage site"
XX Cleavage-site 25..26
XX /note= "BoNT/C sensitive cleavage site"
XX
XX WO2003020948-A2.
XX
XX 13-MAR-2003.
XX
XX 22-AUG-2002; 2002WO-US027145.
XX
XX 28-AUG-2001; 2001US-00942024.
XX
XX (ALLR ) ALLERGAN INC.
XX
XX Steward LE, Fernandez-Salas E, Aoki KR;
XX
XX WPI; 2003-290198/28.
XX
XX Botulinum serotype A/E substrate useful for assaying protease activity of
XX botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
XX toxin recognition sequence that includes a cleavage site.
XX
XX Disclosure; Page 42; 168pp; English.
XX
XX The present invention relates to novel clostridium toxin substrates. The
XX invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
XX which comprise a donor fluorophore, an acceptor having an absorbance
XX spectrum overlapping the emission spectrum of the donor fluorophore and a
XX BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
XX the cleavage site intervenes between the donor fluorophore and acceptor
XX and under the appropriate conditions, the resonance energy transfer is
XX exhibited between the donor and acceptor. Natural targets of clostridium
XX neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
XX of the invention are useful in assaying for the protease activity of any
XX clostridial toxin including botulinum toxins of all serotypes and tetanus
XX toxins (TeNT) in a sample including bacterial, baculoviral and yeast
XX lysate, raw, cooked or processed foods, beverages, animal feed, soil
XX samples, water samples, cosmetics, tissue samples and beverage or food
XX samples. They are useful to assay a sample from a human or animal, for
XX e.g., exposed to clostridial toxin or having one or more symptoms of a
XX clostridial toxin, to follow activity during production and purification
XX of clostridial toxin and to assay formulated clostridial toxin products
XX including pharmaceuticals and cosmetics. The present sequence is SNAP-25
XX peptide used in the invention
XX
XX Sequence 33 AA;
XX
XX Query Match 89.9%; Score 89; DB 6; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4 KTRIDEANQRATKMLGSG 21
XX |||||||
XX 16 KTRIDEANQRATKMLGSG 33
XX
XX RESULT 15
XX AAE36678
XX ID AAE36678 standard; peptide; 33 AA.
XX
XX AC AAE36678;
XX
XX 07-AUG-2003 (first entry)
XX
XX DE SNAP-25 peptide.
XX

```

Search completed: April 3, 2006, 15:36:56
 Job time : 113.992 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:49:32 ; Search time 11.7064 Seconds
(without alignments)
57.210 Million cell updates/sec

Title: US-09-942-098-93

Perfect score: 99

Sequence: 1 XMEKTRIDEANQRATKMLGSGX 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pap.*
- 2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pap.*
- 3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pap.*
- 4: /SIDSS/ptodata/1/pubpaa/PCT_NEW PUB.pap.*
- 5: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pap.*
- 6: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pap.*
- 7: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pap.*
- 8: /SIDSS/ptodata/1/pubpaa/US60 NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	89.9	33	6	US-10-947-071-36
2	89	89.9	33	6	US-10-947-071-40
3	89	89.9	33	6	US-10-947-071-41
4	89	89.9	33	6	US-10-948-097-36
5	89	89.9	33	6	US-10-948-097-40
6	89	89.9	33	6	US-10-948-097-41
7	89	89.9	116	7	US-11-195-098-11
8	89	89.9	203	6	US-10-947-071-4
9	89	89.9	203	6	US-10-948-097-4
10	89	89.9	206	6	US-10-947-071-1
11	89	89.9	206	6	US-10-947-071-2
12	89	89.9	206	6	US-10-948-097-1
13	89	89.9	206	6	US-10-948-097-2
14	89	89.9	206	7	US-11-169-041-225
15	89	89.9	334	6	US-10-947-071-20
16	89	89.9	334	6	US-10-948-097-20
17	83	83.8	116	7	US-11-195-098-12
18	79	79.8	24	7	US-11-195-098-8
19	73	73.7	17	6	US-10-980-346B-6
20	73	73.7	17	6	US-10-980-346B-37
21	73	73.7	17	6	US-10-947-071-33
22	73	73.7	17	6	US-10-948-097-33
23	73	73.7	18	6	US-10-947-071-35
24	73	73.7	18	6	US-10-948-097-35
25	73	73.7	22	6	US-10-980-346B-1

26	70	70.7	17	6	US-10-947-071-61	Sequence 61, Appl
27	70	70.7	17	6	US-10-948-097-61	Sequence 61, Appl
28	69	69.7	16	6	US-10-947-071-32	Sequence 32, Appl
29	69	69.7	16	6	US-10-948-097-32	Sequence 32, Appl
30	69	69.7	17	6	US-10-947-071-34	Sequence 34, Appl
31	69	69.7	17	6	US-10-947-071-53	Sequence 53, Appl
32	69	69.7	17	6	US-10-947-071-55	Sequence 55, Appl
33	69	69.7	17	6	US-10-947-071-60	Sequence 60, Appl
34	69	69.7	17	6	US-10-948-097-34	Sequence 34, Appl
35	69	69.7	17	6	US-10-948-097-53	Sequence 53, Appl
36	69	69.7	17	6	US-10-948-097-55	Sequence 55, Appl
37	69	69.7	17	6	US-10-948-097-60	Sequence 60, Appl
38	68	68.7	17	6	US-10-947-071-54	Sequence 54, Appl
39	68	68.7	17	6	US-10-947-071-58	Sequence 58, Appl
40	68	68.7	17	6	US-10-947-071-62	Sequence 62, Appl
41	68	68.7	17	6	US-10-948-097-54	Sequence 54, Appl
42	68	68.7	17	6	US-10-948-097-58	Sequence 58, Appl
43	68	68.7	17	6	US-10-948-097-62	Sequence 62, Appl
44	67	67.7	17	6	US-10-980-346B-38	Sequence 38, Appl
45	67	67.7	17	6	US-10-947-071-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-10-947-071-36
; Sequence 36, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-947-071-36

Query Match 89.9%; Score 89; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KTRIDEANQRATKMLGSG 21
Db 16 KTRIDEANQRATKMLGSG 33

RESULT 2
US-10-947-071-40
; Sequence 40, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-40

Query Match      89.9%; Score 89; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 16 KTRIDEANQRATKMLGSG 33

RESULT 3
US-10-947-071-41
; Sequence 41, Application US/10947071
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; FILE REFERENCE: 66872-043
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-947-071-41

Query Match      89.9%; Score 89; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 16 KTRIDEANQRATKMLGSG 33

RESULT 4
US-10-948-097-36
; Sequence 36, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-948-097-36

Query Match      89.9%; Score 89; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 16 KTRIDEANQRATKMLGSG 33

RESULT 5
US-10-948-097-40
; Sequence 40, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-40

Query Match      89.9%; Score 89; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 16 KTRIDEANQRATKMLGSG 33

RESULT 6
US-10-948-097-41
; Sequence 41, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; FILE REFERENCE: 66872-040
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-948-097-41

Query Match      89.9%; Score 89; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 16 KTRIDEANQRATKMLGSG 33

RESULT 7
US-11-195-098-11
```

```
; Sequence 11, Application US/11195098
; Publication No. US20050287622A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/11/195,098
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/802,574
; PRIOR FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 09/962,360
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
; US-11-195-098-11

Query Match      89.9%; Score 89; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
Db      98 KTRIDEANQRATKMLGSG 115

RESULT 8
US-10-947-071-4
; Sequence 4, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
; US-10-947-071-4

Query Match      89.9%; Score 89; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
Db      186 KTRIDEANQRATKMLGSG 203

RESULT 9
US-10-948-097-4
; Sequence 11, Application US/11195098
; Publication No. US20050287622A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/11/195,098
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/802,574
; PRIOR FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 09/962,360
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
; US-11-195-098-11

Query Match      89.9%; Score 89; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
Db      98 KTRIDEANQRATKMLGSG 115

RESULT 8
US-10-947-071-4
; Sequence 4, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
; US-10-947-071-4

Query Match      89.9%; Score 89; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
Db      186 KTRIDEANQRATKMLGSG 203

RESULT 9
US-10-948-097-4
; Sequence 11, Application US/11195098
; Publication No. US20050287622A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/11/195,098
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/802,574
; PRIOR FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: 09/962,360
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
; US-11-195-098-11

Query Match      89.9%; Score 89; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
Db      98 KTRIDEANQRATKMLGSG 115

RESULT 8
US-10-947-071-4
; Sequence 4, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-947-071-1

Query Match      89.9%; Score 89; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
Db      189 KTRIDEANQRATKMLGSG 206

RESULT 11
US-10-947-071-2
; Sequence 2, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
```

```
; Sequence 4, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
; US-10-948-097-4

Query Match      89.9%; Score 89; DB 6; Length 203;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
Db      186 KTRIDEANQRATKMLGSG 203

RESULT 10
US-10-947-071-1
; Sequence 1, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-947-071-1

Query Match      89.9%; Score 89; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
Db      189 KTRIDEANQRATKMLGSG 206

RESULT 11
US-10-947-071-2
; Sequence 2, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
```

; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-947-071-2

Query Match 89.9%; Score 89; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 189 KTRIDEANQRATKMLGSG 206
|||||

RESULT 12

US-10-948-097-1

; Sequence 1, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-097-1

Query Match 89.9%; Score 89; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 189 KTRIDEANQRATKMLGSG 206
|||||

RESULT 13

US-10-948-097-2

; Sequence 2, Application US/10948097
; Publication No. US20060063222A1
; GENERAL INFORMATION:
; APPLICANT: Verhagen, Marc
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fluorescence Polarization Assays For
; TITLE OF INVENTION: Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-040
; CURRENT APPLICATION NUMBER: US/10/948,097
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT

; ORGANISM: Mus musculus
US-10-948-097-2

Query Match 89.9%; Score 89; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 189 KTRIDEANQRATKMLGSG 206
|||||

RESULT 14

US-11-169-041-225
; Sequence 225, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 225
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-225

Query Match 89.9%; Score 89; DB 7; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 189 KTRIDEANQRATKMLGSG 206
|||||

RESULT 15

US-10-947-071-20
; Sequence 20, Application US/10947071
; Publication No. US20060063221A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Dudley J.
; APPLICANT: Gilmore, Marcella
; APPLICANT: Steward, Lance
; APPLICANT: Verhagen, Marc
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Lanthanide-Based Substrates and Methods
; TITLE OF INVENTION: For Determining Clostridial Toxin Activity
; FILE REFERENCE: 66872-043
; CURRENT APPLICATION NUMBER: US/10/947,071
; CURRENT FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pQBI GFP-SNAP25
US-10-947-071-20

Query Match 89.9%; Score 89; DB 6; Length 334;
Best Local Similarity 100.0%; Pred. No. 7.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:46:49 ; Search time 94.6606 Seconds
(without alignments)
97.107 Million cell updates/sec

Title: US-09-942-098-93
Perfect score: 99
Sequence: 1 XMEKTRIDEANQRATKMLGSGX 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	100.0	22	3	US-09-942-024-93
2	99	100.0	22	3	US-09-942-098-93
3	89	89.9	23	3	US-09-942-024-88
4	89	89.9	23	3	US-09-942-098-88
5	89	89.9	24	3	US-09-942-024-90
6	89	89.9	24	3	US-09-942-098-90
7	89	89.9	33	3	US-09-942-024-33
8	89	89.9	33	3	US-09-942-024-37
9	89	89.9	33	3	US-09-942-024-38
10	89	89.9	33	3	US-09-942-098-33
11	89	89.9	33	3	US-09-942-098-37
12	89	89.9	33	3	US-09-942-098-38
13	89	89.9	33	4	US-10-261-161-55
14	89	89.9	33	4	US-10-261-161-59
15	89	89.9	33	4	US-10-261-161-60
16	89	89.9	33	5	US-10-917-844-33
17	89	89.9	33	5	US-10-917-844-37
18	89	89.9	33	5	US-10-917-844-38
19	89	89.9	86	4	US-10-705-857-4
20	89	89.9	114	5	US-10-917-844-112
21	89	89.9	116	3	US-09-962-360B-11
22	89	89.9	116	4	US-10-802-574-11
23	89	89.9	203	3	US-09-942-024-14
24	89	89.9	203	3	US-09-942-098-14
25	89	89.9	203	4	US-10-261-161-7
26	89	89.9	203	5	US-10-917-844-14
27	89	89.9	206	3	US-09-942-024-2

28	89	89.9	206	3	US-09-942-024-7	Sequence 7, Appli
29	89	89.9	206	3	US-09-942-024-12	Sequence 12, Appli
30	89	89.9	206	3	US-09-942-098-2	Sequence 2, Appli
31	89	89.9	206	3	US-09-942-098-7	Sequence 7, Appli
32	89	89.9	206	3	US-09-942-098-12	Sequence 12, Appli
33	89	89.9	206	4	US-10-261-161-4	Sequence 4, Appli
34	89	89.9	206	4	US-10-261-161-5	Sequence 5, Appli
35	89	89.9	206	4	US-10-261-161-109	Sequence 109, Appl
36	89	89.9	206	4	US-10-318-417-3	Sequence 3, Appli
37	89	89.9	206	5	US-10-723-860-1223	Sequence 1223, Ap
38	89	89.9	206	5	US-10-917-844-2	Sequence 2, Appli
39	89	89.9	206	5	US-10-917-844-12	Sequence 12, Appli
40	89	89.9	206	5	US-10-917-844-90	Sequence 90, Appli
41	89	89.9	206	5	US-10-756-149-5012	Sequence 5012, Ap
42	89	89.9	333	5	US-10-917-844-86	Sequence 86, Appl
43	89	89.9	347	5	US-10-917-844-88	Sequence 88, Appli
44	84	84.8	19	3	US-09-942-024-92	Sequence 92, Appli
45	84	84.8	19	3	US-09-942-024-95	Sequence 95, Appli

ALIGNMENTS

RESULT 1
US-09-942-024-93
; Sequence 93, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa-fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 22
; OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-93

Query Match 100.0%; Score 99; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MEKTRIDEANQRATKMLGSG 21
Db 2 MEKTRIDEANQRATKMLGSG 21

RESULT 2
US-09-942-098-93
; Sequence 93, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial

```
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 22
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
;
US-09-942-098-93
```

```
Query Match 100.0%; Score 99; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MEKTRIDEANQRATKMLGSG 21
| | | | | | | | | | | | | | | | | | | |
Db 2 MEKTRIDEANQRATKMLGSG 21
```

```
RESULT 3
US-09-942-024-88
; Sequence 88, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 23
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
;
US-09-942-024-88
```

```
Query Match 89.9%; Score 89; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KTRIDEANQRATKMLGSG 21
| | | | | | | | | | | | | | | | | | | |
Db 5 KTRIDEANQRATKMLGSG 22
```

```
RESULT 4
US-09-942-098-88
; Sequence 88, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 23
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
;
US-09-942-098-88
```

```
Query Match 89.9%; Score 89; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KTRIDEANQRATKMLGSG 21
| | | | | | | | | | | | | | | | | | | |
Db 5 KTRIDEANQRATKMLGSG 22
```

```
RESULT 5
US-09-942-024-90
; Sequence 90, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 24
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
;
US-09-942-024-90
```

Query Match 89.9%; Score 89; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
 |||||
 Db 6 KTRIDEANQRATKMLGSG 23

RESULT 6
 US-09-942-098-90
 ; Sequence 90, Application US/09942098
 ; Publication No. US20030143651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steward, Lance E.
 ; APPLICANT: Fernandez-Salas, Ester
 ; APPLICANT: Aoki, Kei Roger
 ; TITLE OF INVENTION: Fret Protease Assays For Clostridial
 ; TITLE OF INVENTION: Toxins
 ; FILE REFERENCE: P-AR 4802
 ; CURRENT APPLICATION NUMBER: US/09/942,098
 ; CURRENT FILING DATE: 2001-08-28
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 90
 ; LENGTH: 24
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic peptide
 ; NAME/KEY: MOD_RES
 ; LOCATION: 1
 ; OTHER INFORMATION: Xaa=fluorescein-modified lysine
 ; NAME/KEY: MOD_RES
 ; LOCATION: 24
 ; NAME/KEY: AMIDATION
 ; LOCATION: (O)...(O)
 ; OTHER INFORMATION: at the C-terminal
 US-09-942-098-90

Query Match 89.9%; Score 89; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
 |||||
 Db 6 KTRIDEANQRATKMLGSG 23

RESULT 7
 US-09-942-024-33
 ; Sequence 33, Application US/09942024
 ; Publication No. US20030143650A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steward, Lance E.
 ; APPLICANT: Fernandez-Salas, Ester
 ; APPLICANT: Aoki, Kei Roger
 ; TITLE OF INVENTION: Fret Protease Assays For Botulinum
 ; TITLE OF INVENTION: Serotype A/E Toxins
 ; FILE REFERENCE: P-AR 4803
 ; CURRENT APPLICATION NUMBER: US/09/942,024
 ; CURRENT FILING DATE: 2001-08-28
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 33
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-942-024-33

Query Match 89.9%; Score 89; DB 3; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KTRIDEANQRATKMLGSG 21
 |||||
 Db 16 KTRIDEANQRATKMLGSG 33

RESULT 8
 US-09-942-024-37
 ; Sequence 37, Application US/09942024
 ; Publication No. US20030143650A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steward, Lance E.
 ; APPLICANT: Fernandez-Salas, Ester
 ; APPLICANT: Aoki, Kei Roger
 ; TITLE OF INVENTION: Fret Protease Assays For Botulinum
 ; TITLE OF INVENTION: Serotype A/E Toxins
 ; FILE REFERENCE: P-AR 4803
 ; CURRENT APPLICATION NUMBER: US/09/942,024
 ; CURRENT FILING DATE: 2001-08-28
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 37
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Carassius auratus
 US-09-942-024-37

Query Match 89.9%; Score 89; DB 3; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
 |||||
 Db 16 KTRIDEANQRATKMLGSG 33

RESULT 9
 US-09-942-024-38
 ; Sequence 38, Application US/09942024
 ; Publication No. US20030143650A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steward, Lance E.
 ; APPLICANT: Fernandez-Salas, Ester
 ; APPLICANT: Aoki, Kei Roger
 ; TITLE OF INVENTION: Fret Protease Assays For Botulinum
 ; TITLE OF INVENTION: Serotype A/E Toxins
 ; FILE REFERENCE: P-AR 4803
 ; CURRENT APPLICATION NUMBER: US/09/942,024
 ; CURRENT FILING DATE: 2001-08-28
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 38
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Carassius auratus
 US-09-942-024-38

Query Match 89.9%; Score 89; DB 3; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
 |||||
 Db 16 KTRIDEANQRATKMLGSG 33

RESULT 10
 US-09-942-098-33
 ; Sequence 33, Application US/09942098
 ; Publication No. US20030143651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steward, Lance E.

```
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-33

Query Match      89.9%; Score 89; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
      |||
Db      16 KTRIDEANQRATKMLGSG 33

RESULT 13
US-10-261-161-55
; Sequence 55, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-261-161-55

Query Match      89.9%; Score 89; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
      |||
Db      16 KTRIDEANQRATKMLGSG 33

RESULT 14
US-10-261-161-59
; Sequence 59, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-261-161-59

Query Match      89.9%; Score 89; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
      |||
Db      16 KTRIDEANQRATKMLGSG 33

RESULT 15
US-10-261-161-60

; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-33

Query Match      89.9%; Score 89; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
      |||
Db      16 KTRIDEANQRATKMLGSG 33

RESULT 11
US-09-942-098-37
; Sequence 37, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-098-37

Query Match      89.9%; Score 89; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
      |||
Db      16 KTRIDEANQRATKMLGSG 33

RESULT 12
US-09-942-098-38
; Sequence 38, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
```

; Sequence 60, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-10-261-161-60

Query Match 89.9%; Score 89; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KTRIDEANQRATKMLGSG 21
| | | | | | | | | | | | | | | | | | | | | |
Db 16 KTRIDEANQRATKMLGSG 33

Search completed: April 3, 2006, 15:57:05
Job time : 94.6606 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 3, 2006, 15:31:39 ; Search time 17.5596 Seconds
(without alignments)
103.582 Million cell updates/sec

Title: US-09-942-098-93

Perfect score: 99

Sequence: 1 XMEKTRIDEANQRATKMLGSGX 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pdp:*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pdp:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pdp:*
4: /cgn2_6/ptodata/1/iaa/PCRU5 COMB.pdp:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pdp:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	89.9	20	2	US-08-819-286-9
2	89	89.9	26	2	US-08-819-286-8
3	89	89.9	37	2	US-08-819-286-4
4	89	89.9	70	1	US-08-760-001-10
5	89	89.9	70	2	US-09-015-960-10
6	89	89.9	70	2	US-09-534-572-10
7	89	89.9	116	2	US-09-962-360B-11
8	89	89.9	206	1	US-08-393-985-18
9	89	89.9	206	2	US-08-819-286-1
10	89	89.9	206	2	US-09-949-016-6311
11	89	89.9	219	2	US-09-949-016-10671
12	83	83.8	116	2	US-09-962-360B-12
13	79	79.8	24	2	US-09-962-360B-8
14	73	73.7	17	1	US-08-743-894B-1
15	73	73.7	17	1	US-08-743-894B-37
16	70	70.7	17	1	US-08-743-894B-18
17	70	70.7	17	1	US-08-743-894B-43
18	69	69.7	16	1	US-08-743-894B-49
19	69	69.7	17	1	US-08-743-894B-27
20	69	69.7	17	1	US-08-743-894B-30
21	69	69.7	17	1	US-08-743-894B-32
22	69	69.7	17	1	US-08-743-894B-39
23	68	68.7	17	1	US-08-743-894B-19
24	68	68.7	17	1	US-08-743-894B-25
25	68	68.7	17	1	US-08-743-894B-29
26	68	68.7	17	1	US-08-743-894B-42
27	68	68.7	17	1	US-08-743-894B-50

28	67	67.7	17	1	US-08-743-894B-2	Sequence 2, Appli
29	67	67.7	17	1	US-08-743-894B-20	Sequence 20, Appl
30	67	67.7	17	1	US-08-743-894B-24	Sequence 24, Appl
31	67	67.7	17	1	US-08-743-894B-26	Sequence 26, Appl
32	67	67.7	17	1	US-08-743-894B-28	Sequence 28, Appl
33	67	67.7	17	1	US-08-743-894B-31	Sequence 31, Appl
34	67	67.7	17	1	US-08-743-894B-33	Sequence 33, Appl
35	67	67.7	17	1	US-08-743-894B-34	Sequence 34, Appl
36	67	67.7	17	1	US-08-743-894B-36	Sequence 36, Appl
37	67	67.7	17	1	US-08-743-894B-44	Sequence 44, Appl
38	67	67.7	17	1	US-08-743-894B-45	Sequence 45, Appl
39	67	67.7	17	1	US-08-743-894B-46	Sequence 46, Appl
40	65	65.7	17	1	US-08-743-894B-21	Sequence 21, Appl
41	65	65.7	17	1	US-08-743-894B-35	Sequence 35, Appl
42	65	65.7	17	1	US-08-743-894B-47	Sequence 47, Appl
43	65	65.7	17	1	US-08-743-894B-48	Sequence 48, Appl
44	64	64.6	13	2	US-09-976-535A-1	Sequence 1, Appli
45	64	64.6	15	1	US-08-743-894B-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-08-819-286-9
; Sequence 9, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Mortal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-9

Query Match 89.9%; Score 89; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
|||||

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-760-001-10

Query Match 89.9%; Score 89; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 6.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 53 KTRIDEANQRATKMLGSG 70

RESULT 5
US-09-015-960-10
Sequence 10, Application US/09015960
Patent No. 6043042
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,960
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-015-960-10

Query Match 89.9%; Score 89; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 6.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 53 KTRIDEANQRATKMLGSG 70

RESULT 6
US-09-534-572-10
Sequence 10, Application US/09534572
Patent No. 6337386
GENERAL INFORMATION:
APPLICANT: Shone, Clifford C.
APPLICANT: Hallis, Bassam
APPLICANT: James, Benjamin A. F.
APPLICANT: Quinn, Conrad P.
TITLE OF INVENTION: TOXIN ASSAY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,572
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/015,960
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,001
FILING DATE: 30-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01279
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0120003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-534-572-10

Query Match 89.9%; Score 89; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 6.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 53 KTRIDEANQRATKMLGSG 70

RESULT 7
US-09-962-360B-11
Sequence 11, Application US/09962360B
Patent No. 6762280
GENERAL INFORMATION:
APPLICANT: Schmidt, James J.
APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
FILE REFERENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US/09/962,360B

```

; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT E
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-09-962-360B-11

Query Match          89.9%; Score 89; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 KTRIDEANQRATKMLGSG 21
DB      98 KTRIDEANQRATKMLGSG 115

RESULT 8
US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Scheller, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: Of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-393-985-18

Query Match          89.9%; Score 89; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 KTRIDEANQRATKMLGSG 21
DB      189 KTRIDEANQRATKMLGSG 206

```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6311
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6311

Query Match      89.9%; Score 89; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
      |||||
Db      189 KTRIDEANQRATKMLGSG 206

RESULT 11
US-09-949-016-10671
; Sequence 10671, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10671
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10671

Query Match      89.9%; Score 89; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
      |||||
Db      202 KTRIDEANQRATKMLGSG 219

RESULT 12
US-09-962-360B-12
; Sequence 12, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 12
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT E
US-09-949-016-10671

```

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is S-fluoresceinyl-cysteine
US-09-962-360B-12

Query Match      83.8%; Score 83; DB 2; Length 116;
Best Local Similarity 94.4%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
      |||||
Db      98 KTRIDEANQRATKMLGSG 115

RESULT 13
US-09-962-360B-8
; Sequence 8, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 8
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT A
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is N-fluoresceinyl-glycine
US-09-962-360B-8

Query Match      79.8%; Score 79; DB 2; Length 24;
Best Local Similarity 83.3%; Pred. No. 9.6e-07;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      4 KTRIDEANQRATKMLGSG 21
      |||||
Db      6 KTRIDEANQRATKMLGSG 23

RESULT 14
US-08-743-894B-1
; Sequence 1, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn: John Moran-Patent Atty
; STREET: USA WPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
US-08-743-894B-1

```

```

; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
US-08-743-894B-1
Query Match 73.7%; Score 73; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 KTRIDEANQRATKML 18
   |||||
DB 3 KTRIDEANQRATKML 17

```

```

RESULT 15
US-08-743-894B-37
; Sequence 37, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MEMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;

```

```

; FEATURE:
; US-08-743-894B-37
Query Match 73.7%; Score 73; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 KTRIDEANQRATKML 18
   |||||
DB 3 KTRIDEANQRATKML 17
Search completed: April 3, 2006, 15:33:15
Job time : 18.5596 secs

```

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	89	89.9	124	2	Q93578	BRARE	Q93578 brachydanio
2	89	89.9	134	2	Q4S8B5	TEYNG	Q4S8B5 tetraodon n
3	89	89.9	143	2	Q9GM34	MACFA	Q9GM34 macaca fasc
4	89	89.9	198	2	Q6PC84	BRARE	Q6PC84 brachydanio
5	89	89.9	203	1	SN25B	CARAU	SN25B carassius a
6	89	89.9	203	2	Q93579	BRARE	Q93579 brachydanio
7	89	89.9	203	2	Q6PC54	BRARE	Q6PC54 brachydanio
8	89	89.9	204	1	SN25A	CARAU	SN25A carassius a
9	89	89.9	204	2	Q705J6	LATYA	Q705J6 lateolabrax
10	89	89.9	204	2	Q5T266	BRARE	Q5T266 brachydanio
11	89	89.9	204	2	Q5T265	BRARE	Q5T265 brachydanio
12	89	89.9	206	1	SNP25	CHICK	SNP25 gallus gall
13	89	89.9	206	1	SNP25	HUMAN	SNP25 homo sapien
14	89	89.9	206	1	SNP25	MACMU	SNP25 macaca mula
15	89	89.9	206	1	SNP25	MOUSE	SNP25 mus musculu
16	89	89.9	206	1	SNP25	PANTR	SNP25 pan troglod
17	89	89.9	206	1	SNP25	RAT	SNP25 rattus norv
18	89	89.9	206	2	Q53EM2	HUMAN	Q53EM2 homo sapien
19	89	89.9	206	2	Q5U0B5	HUMAN	Q5U0B5 homo sapien
20	89	89.9	206	2	Q5NVG5	PONPY	Q5NVG5 pongo pygma
21	89	89.9	206	2	Q5NVK3	PONPY	Q5NVK3 pongo pygma
22	89	89.9	206	2	Q5R690	PONPY	Q5R690 pongo pygma
23	89	89.9	206	2	Q5R6U7	PONPY	Q5R6U7 pongo pygma
24	89	89.9	206	2	Q4RU46	MACFA	Q4RU46 macaca fasc
25	89	89.9	236	2	Q4V509	CARAU	Q4V509 carassius a
26	85	85.9	204	2	Q6P317	BRARE	Q6P317 brachydanio
27	82	82.8	206	2	Q5R505	PONPY	Q5R505 pongo pygma
28	75	75.8	206	2	Q640M4	XENLA	Q640M4 xenopus lae
29	75	75.8	206	2	Q8AXM1	XENLA	Q8AXM1 xenopus lae
30	75	75.8	206	2	Q8AXM2	XENLA	Q8AXM2 xenopus lae
31	65	65.7	214	2	Q7ZVE4	BRARE	Q7ZVE4 brachydanio

```

Q4S8B5_TETNG
ID Q4S8B5_TETNG PRELIMINARY; PRT; 134 AA.
AC Q4S8B5_2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome-undetermined SCAF14706, whole genome shotgun sequence.
GN ORFNAMES=GSTENG0022427001;
DE Tetraodon nigroviridis (Green puffer).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
NUCLEOTIDE SEQUENCE.
RP RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Bottolico L., Poulain J., De Berardinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
NUCLEOTIDE SEQUENCE.
RP RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014706; GAG03117.1; -; Genomic DNA.
SQ SEQUENCE 134 AA; 14682 MW; 09109FF243890AB8 CRC64;

Query Match 89.9%; Score 89; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 117 KTRIDEANQRATKMLGSG 134
|||||
|||||

RESULT 3
Q9GM34_MACFA
ID Q9GM34_MACFA PRELIMINARY; PRT; 143 AA.
AC Q9GM34;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
NUCLEOTIDE SEQUENCE.
RP RC TISSUE=Brain parietal lobe;
RA Oada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049852; BAB16738.1; -; mRNA.
DR HSSP; Q8T3S4; 1L4A.

```

```

DR SMR; Q9GM34; 68-141.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 1.
DR PROSITE; PS50192; T_SNARE; 1.
KW Hypothetical protein; Synaptosome.
SQ SEQUENCE 143 AA; 16043 MW; D625DBAAA0893FB0 CRC64;

Query Match 89.9%; Score 89; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 126 KTRIDEANQRATKMLGSG 143
|||||
|||||

RESULT 4
Q6PC84_BRARE
ID Q6PC84_BRARE PRELIMINARY; PRT; 198 AA.
AC Q6PC84;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Snap25a protein.
GN Name=snap25a;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
NUCLEOTIDE SEQUENCE.
RP RC STRAIN=Wild-type; TISSUE=Eye;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
NUCLEOTIDE SEQUENCE.
RP RC STRAIN=Wild-type; TISSUE=Eye;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059439; AAH59439.1; -; mRNA.
DR SMR; Q6PC84; 1-77, 123-196.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 1.
DR PROSITE; PS50192; T_SNARE; 2.

```

KW Synaptosome.
SQ SEQUENCE 198 AA; 22209 MW; 8FED5099A00E1EC0 CRC64;
Query Match 89.9%; Score 89; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 KTRIDEANORATKMLGSG 21
Db 181 KTRIDEANORATKMLGSG 198
RESULT 5
SN25B CARAU STANDARD; PRT; 203 AA.
AC P36978;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptosomal-associated protein 25B (SNAP-25B).
GN Name=SNAP-B;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RX MEDLINE=94068448; PubMed=8248151;
RA Rasinger C., Larhammar D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish."
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC -!- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of the nerve terminal.
CC -!- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, and piriform cortex, anterior thalamic nuclei, pontine nuclei, and granule cells of the cerebellum.
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL; L22976; AAA16538.1; -; mRNA.
CC PIR; I50481; I50481.
CC HSSP; P13795; 1SFC.
DR SMR; P36978; 7-82, 128-201.
DR InterPro; IPR00528; SNAP-25.
DR InterPro; IPR000727; t-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; t-SNARE; 2.
KW Coiled coil; Glycoprotein; Multigene family; Repeat; Synaptosome.
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 137 199 t-SNARE coiled-coil homology 2.
FT COMPBIAS 85 92 Cys-rich.
FT CARBOHYD 77 97 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 185 185 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 203 AA; 22664 MW; 8DFEBE8ED37D6D7 CRC64;
Query Match 89.9%; Score 89; DB 1; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KTRIDEANORATKMLGSG 21
Db 186 KTRIDEANORATKMLGSG 203
RESULT 6
O93579 BRARE PRELIMINARY; PRT; 203 AA.
AC O93579;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein 25.2.
GN Name=snap25b; Synonyms=Snap;
OS Brachydanio rerio (Zebrafish)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99057281; PubMed=9843147;
RX DOI=10.1002/(SICI)1097-4547(19981201)54:5<563::AID-JNRL13.3.CO;2-2;
RA Rasinger C., Salanek E., Soderberg C., Gates M., Postlethwait J.H., Larhammar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish: comparison of paralogous linkage groups suggests loss of one locus in the mammalian lineage."
RL J. Neurosci. Res. 54:563-573(1998).
DR EMBL; AF091594; AAC64290.1; -; mRNA.
DR HSSP; P60881; IUTH.
DR SMR; O93579; 7-82, 128-201.
DR ZFIN; ZDB-GENE-980526-392; snap25b.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; t-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; t-SNARE; 2.
KW Synaptosome.
SQ SEQUENCE 203 AA; 22647 MW; 93B7590DD0C93F38 CRC64;
Query Match 89.9%; Score 89; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 KTRIDEANORATKMLGSG 21
Db 186 KTRIDEANORATKMLGSG 203
RESULT 7
Q6PC54 BRARE PRELIMINARY; PRT; 203 AA.
AC Q6PC54;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Synaptosome-associated protein 25 b.
GN Name=snap25b;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wild-type; TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.N., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Wild-type; TISSUE=Eye;
RA Strauberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC059469; AAH59469.1; -; mRNA.
DR SNR; Q6PC54; 7-82, 128-201.
DR ZFIN; ZDB-GENE-980526-392; snap25b.
GO: GO:0019717; C:synaposome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; t-SNARE; 2.
KW Synaposome.
SQ SEQUENCE 203 AA; 22693 MW; 48D7590DD0C1179A CRC64;

Query Match 89.9%; Score 89; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 186 KTRIDEANQRATKMLGSG 203
|||||

RESULT 8
ID SN25A_CARAU STANDARD; PRT; 204 AA.
AC P36977;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaposomal-associated protein 25A (SNAP-25A).
GN Name=SNAP-A;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RX MEDLINE=94068448; PubMed=8248151;
RA Risinger C., Latham D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid
RT goldfish.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC -|- FUNCTION: May play an important role in the synaptic function of
CC specific neuronal systems. Associates with proteins involved in
CC vesicle docking and membrane fusion.
CC -|- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
CC the nerve terminal.
CC -|- SIMILARITY: Belongs to the SNAP-25 family.
CC -|- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; L22973; AAA16537.1; -; mRNA.
DR PIR; I50480; I50480.
DR HSSP; P13795; 1N7S.
DR SNR; P36977; 7-83, 129-202.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; T-SNARE; 2.
KW Coiled coil; Multigene family; Repeat; Synaposome.
FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
FT DOMAIN 138 200 t-SNARE coiled-coil homology 2.
FT COMPBIAS 85 92 Cys-rich.
SQ SEQUENCE 204 AA; 22843 MW; 458BBECFCFC09189 CRC64;

Query Match 89.9%; Score 89; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 187 KTRIDEANQRATKMLGSG 204
|||||

RESULT 9
ID Q705J6_LATJA PRELIMINARY; PRT; 204 AA.
AC Q705J6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Synaposomal-associated protein 25.
GN Name=snap-25;
OS Lateolabrax japonicus (Japanese sea perch) (Japanese sea bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Lateolabrax.
OX NCBI_TaxID=8164;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Chen K., Huang X.H.;
RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ619993; CAF04071.1; -; mRNA.
DR SNR; Q705J6; 7-83, 129-202.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; T-SNARE; 2.
SQ SEQUENCE 204 AA; 22842 MW; 8F77B18D591509B2 CRC64;

Query Match 89.9%; Score 89; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 187 KTRIDEANQRATKMLGSG 204
|||||

```
RESULT 10
Q5TZ66 BRARE
ID Q5TZ66 BRARE PRELIMINARY; PRT; 204 AA.
AC Q5TZ66;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Synaptosomal-associated protein (SNAP).
GN Name=snap25a; Synonyms=OTDARP0000005690; ORFNames=DKEYP-8P4.6-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lovell J.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Donaldson S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX465184; CAH69031.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69031.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69031.1; JOINED; Genomic DNA.
DR EMBL; BX465184; CAI21360.1; JOINED; Genomic DNA.
DR SMR; Q5TZ66; 7-83, 129-202.
DR Ensemble; ENSDARG00000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR Pfam; PF00835; SNAP-25; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; t_SNARE; 2.
KW Synaptosome.
SQ SEQUENCE 204 AA; 22857 MW; B53CF5D3D1C69EA5 CRC64;

Query Match 89.9%; Score 89; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 187 KTRIDEANQRATKMLGSG 204

RESULT 11
Q5TZ65 BRARE
ID Q5TZ65 BRARE PRELIMINARY; PRT; 204 AA.
AC Q5TZ65;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Synaptosomal-associated protein (SNAP)
GN Name=snap25a; Synonyms=OTDARP0000005690; ORFNames=DKEYP-8P4.6-002;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lovell J.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Donaldson S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX465184; CAH69032.1; -; Genomic DNA.
DR EMBL; BX470246; CAI21360.1; -; Genomic DNA.
DR EMBL; BX470246; CAH69032.1; JOINED; Genomic DNA.
```

```
DR EMBL; BX465184; CAI21360.1; JOINED; Genomic DNA.
DR SMR; Q5TZ65; 7-83, 129-202.
DR Ensemble; ENSDARG00000020609; Danio rerio.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR GO; GO:0019717; C:synaptosome; IEA.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; t_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR SMART; SM00397; t_SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; t_SNARE; 2.
KW Synaptosome.
SQ SEQUENCE 204 AA; 22878 MW; FBC79AB7015AC0ED CRC64;

Query Match 89.9%; Score 89; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATKMLGSG 21
Db 187 KTRIDEANQRATKMLGSG 204

RESULT 12
SNP25_CHICK
ID SNP25_CHICK STANDARD; PRT; 206 AA.
AC P60878; P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
25 kDa protein) (Super protein) (SUP).
GN Name=SNAP25; Synonyms=SNAP;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM SNAP25B).
RC STRAIN=White leghorn; TISSUE=Retina;
RX MEDLINE=91126080; PubMed=1992470;
RA Catsicas S.; Larhammar D.; Blomqvist A.G.; Sanna P.P.; Milner R.J.;
RA Wilson M.C.;
RA "Expression of a conserved cell-type-specific protein in nerve
terminals coincides with synaptogenesis.";
RT Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
RL [2]
RN NUCLEOTIDE SEQUENCE (ISOFORMS SNAP25A AND SNAP25B).
RP MEDLINE=93389738; PubMed=8377193;
RA Bark I.C.;
RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon
encoding distinct isoforms of the protein.";
RL J. Mol. Biol. 233:67-76(1993).
CC -1- FUNCTION: t-SNARE involved in the molecular regulation of
neurotransmitter release. May play an important role in the
synaptic function of specific neuronal systems. Associates with
proteins involved in vesicle docking and membrane fusion (By
similarity).
CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1
and SNAP25BP. Binds STXBP6. Found in a ternary complex with STX1A
and VAMP8 (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=isoforms differ by the usage of two alternative
homologous exons (5a and 5b) which encode for positions 56 to 94
and differ only in 9 positions out of 39;
Name=SNAP-25b;
IsoId=P60878-1, P13795-1;
Sequence=Displayed;
Name=SNAP-25a;
IsoId=P60878-2, P13795-2;
```


Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Kzywinski M.I., Skalek U., Smailus D.E., Schnerich A., Schein J.E., Jones S.J.M., Marra M.A.; RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [6].

RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 11-81 AND 141-202 IN COMPLEX WITH STX1A, CPLX1 AND VAMP2, AND NMR ANALYSIS.

RX MEDLINE=21822661; PubMed=11832227; DOI=10.1016/S0896-6273(02)00583-4; Chen X., Tomchick D.R., Kovrig E., Arac D., Machius M., Suedhof T.C., Rizo J.; "Three-dimensional structure of the complexin/SNARE complex."; Neuron 33:397-409(2002).

CC -1- FUNCTION: t-SNARE involved in the molecular regulation of neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.

CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2 and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1, SNAP25BP and HGS. Binds STXB6. Found in a ternary complex with STX1A and VAMP8 (By similarity).

CC -1- INTERACTION: QBIUH5:HIP14; NbExp=1; IntAct=EBI-524785, EBI-524753; Event=Alternative splicing; Named isoforms=2; homologous exons (5a and 5b) which encode for positions 56 to 94 and differ only in 9 positions out of 39; Name=SNAP-25b; IsoId=P60880-1, P13795-1; Sequence=Displayed; Name=SNAP-25a; IsoId=P60880-2, P13795-2; Sequence=VSP_006186;

CC -1- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, and piriform cortex, anterior thalamic nuclei, pontine nuclei, and granule cells of the cerebellum.

CC -1- PTM: Palmitoylated (By similarity).

CC -1- SIMILARITY: Belongs to the SNAP-25 family.

CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

EMBL; L19760; AAC37545.1; -; mRNA.

EMBL; L19761; AAC37546.1; -; mRNA.

EMBL; D21267; BAA22370.1; -; mRNA.

EMBL; AL023913; CAC34534.1; -; Genomic DNA.

EMBL; AL023913; CAC34535.1; -; Genomic DNA.

EMBL; AL023913; CAD56158.1; -; Genomic DNA.

EMBL; AL023913; CAB42860.1; -; Genomic DNA.

EMBL; BC010647; AAH10647.1; -; mRNA.

PIR; I53735; I53735.

PIR; I67823; I67823.

PDB; 1KIL; X-ray; C=11-80, D=141-203.

PDB; 1XTG; X-ray; B=146-204.

SMR; P60880; 7-83, 131-204.

IntAct; P60880; -.

ENSEMBL; ENSG00000132639; Homo sapiens.

DR HGNC; HGNC:11132; SNAP25.

DR H-InvDB; HIX0015639; -.

DR MIM; 600322; -.

DR GO; GO:0007269; P:neurotransmitter secretion; NAS.

DR GO; GO:0001504; P:neurotransmitter uptake; NAS.

DR GO; GO:0050796; P:regulation of insulin secretion; TAS.

DR GO; GO:0007268; P:synaptic transmission; NAS.

DR GO; GO:0016081; P:synaptic vesicle docking during exocytosis; NAS.

DR InterPro; IPR000928; SNAP-25.

DR InterPro; IPR000727; T_SNARE.

DR Pfam; PF00835; SNAP-25; 1.

DR Pfam; PF05739; SNARE; 1.

DR SMART; SM00397; t-SNARE; 2.

DR PROSITE; PS0192; t-SNARE; 2.

KW 3D-structure; Alternative splicing; Coiled coil; Lipoprotein;

KW Palmitate; Phosphorylation; Repeat; Synaptosome.

FT DOMAIN 19 81

FT t-SNARE coiled-coil homology 1.

FT COMBIAS 85 92

FT SITE 180 181

FT MOD_RES 138 138

FT MOD_RES 187 187

FT VARSPLIC 58 89

FT SNAP-25a.

FT /FTId=VSP_006186.

FT HELIX 7 82

FT HELIX 142 201

FT TURN 202 202

SQ SEQUENCE 206 AA; 23315 MW; FBED2B082A4CB6A6 CRC64;

Query Match 89.9%; Score 89; DB 1; Length 206;

Best Local Similarity 100.0%; Pred. No. 6.5e-06;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTRIDEANQRATRLGSG 21

|||||

DB 189 KTRIDEANQRATRLGSG 206

RESULT 14

SNP25 MACMU STANDARD; PRT; 206 AA.

AC P60877; P13795; P36974; P70557; P70558; Q81XX3; Q96FM2; Q9BR45;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated 25 kDa protein).

GN Name=SNAP25;

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.

OC NCBI_TaxID=9544;

OX [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Hippocampus;

RA Jensen M.J., Smith L.A.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: t-SNARE involved in the molecular regulation of neurotransmitter release. May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion (By similarity).

CC -1- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2 and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1, SNAP25BP and HGS. Binds STXB6. Found in a ternary complex with STX1A and VAMP8 (By similarity).

CC -1- PTM: Palmitoylated (By similarity).

CC -1- SIMILARITY: Belongs to the SNAP-25 family.

CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

EMBL; AF240770; AAF64477.1; -; mRNA.

SMR; P60877; 7-83, 131-204.

DR InterPro; IPR000928; SNAP-25.

DR InterPro; IPR000727; T_SNARE.

DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t_SNARE; 2.
 DR PROSITE; PS00192; t_SNARE; 2.
 KW Coiled coil; Lipoprotein; Palmitate; Phosphorylation; Repeat;
 KW Synaptosome.
 FT DOMAIN 19 81 t-SNARE coiled-coil homology 1.
 FT DOMAIN 140 202 t-SNARE coiled-coil homology 2.
 FT COMPIAS 85 92 Cys-rich.
 FT SITE 180 181 Cleavage (by BONT/E) (By similarity).
 FT MOD_RES 138 138 Phosphothreonine (By similarity).
 FT MOD_RES 187 187 Phosphoserine (By similarity).
 SQ SEQUENCE 206 AA; FBED2B082A4CB6A6 CRC64;
 Query Match 89.9%; Score 89; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 6.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KTRIDEANQRATKMLGSG 21
 DB 189 KTRIDEANQRATKMLGSG 206
 RESULT 15
 ID SNP25_MOUSE STANDARD; PRT; 206 AA.
 AC P60879; P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Synaptosomal-associated protein 25 (SNAP-25) (Synaptosomal-associated
 DE 25 kDa protein) (Super protein) (SUP).
 DE Names=Snap25; Synonyms=Snap;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM SNAP-25A).
 RC STRAIN=BALB/c;
 RX MEDLINE=90078337; PubMed=2592413; DOI=10.1083/jcb.109.6.3039;
 RA Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,
 RA Bloom F.E., Wilson M.C.;
 RT "The identification of a novel synaptosomal-associated protein, SNAP-
 RT 25, differentially expressed by neuronal subpopulations.";
 RL J. Cell Biol. 109:3039-3052(1989).
 RN [2]
 RP NUCLEOTIDE SEQUENCE (ISOFORM SNAP-25B).
 RC STRAIN=iUS, and ISS;
 RX MEDLINE=2136810; PubMed=11471062; DOI=10.1007/s00335-001-1001-x;
 RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
 RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
 RT "High-throughput sequence identification of gene coding variants
 RT within alcohol-related QTLs.";
 RL Mamm. Genome 12:657-663 (2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25B).
 RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Furuno M., Saio R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt T.A., Brusaic V., Clothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Haeihirume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki K., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM SNAP-25A).
 RC STRAIN=C57BL/6; TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [5]
 RP INTERACTION WITH SNAP25BP.
 RX PubMed=10195194; DOI=10.1038/5673;
 RA Ilardi J.M., Mochida S., Sheng Z.-H.;
 RT "Snapin: a SNARE-associated protein implicated in synaptic
 RT transmission.";
 RL Nat. Neurosci. 2:119-124 (1999).
 RN [6]
 RP PHOSPHORYLATION SITES THR-138 AND SER-187.
 RX MEDLINE=22347237; PubMed=12459461; DOI=10.1016/S0014-5793 (02) 03629-3;
 RA Hepp R., Cabanillo J.P., Roche P.A.;
 RT "Differential phosphorylation of SNAP-25 in vivo by protein kinase C
 RT and protein kinase A.";
 RL FEBS Lett. 532:52-56 (2002).
 CC -I- FUNCTION: t-SNARE involved in the molecular regulation of
 CC neurotransmitter release. May play an important role in the
 CC synaptic function of specific neuronal systems. Associates with
 CC proteins involved in vesicle docking and membrane fusion.
 CC -I- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
 CC and STX1A. This complex binds CPLX1. Interacts with TRIM9, RIMS1,
 CC SNAP25BP and HGS. Binds STXBP6. Found in a ternary complex with
 CC STX1A and VAMP8 (By similarity).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=isoforms differ by the usage of two alternative
 CC homologous exons (5a and 5b) which encode for positions 56 to 94
 CC and differ only in 9 positions out of 39;
 CC Name=SNAP-25b;
 CC IsoId=P60879-1, P13795-1;
 CC Sequence=Displayed;
 CC Name=SNAP-25a;
 CC IsoId=P60879-2, P13795-2;
 CC Sequence=VSP_010019;

Search completed: April 3, 2006, 15:46:24
Job time : 114.431 secs

THIS PAGE BLANK (USPTO)